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The Aged Microenvironment Influences Prostate Carcinogenesis

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14. ABSTRACT The most important single risk factor associated with prostate cancer is advanced age. Despite the strong correlation between aging and prostate cancer, the mechanism(s) underlying this relationship remains unknown. In this study, we quantitated histological and molecular alterations of the mouse prostatic stroma that associate with normal aging in vivo. In a comparison of young (4 month) and old (20-24 month) mice, we identified significant changes in the expression of 1259 genes (p<0.05) in the prostatic stroma that associated with normal aging in vivo. These included over-expression of genes associated with inflammation (e.g., Ccl8, Ccl12), genotoxic/oxidative stress (e.g., Apod, Serpinb5) and soluble factors (e.g., Cyr61) and, down-regulation of pro-collagen genes (e.g., Col1a1 and Col3a1). We demonstrated that aged prostates exhibit a disrupted collagenous matrix and aged collagen induced the invasion of prostate cancer cells in vitro. Immunohistochemical studies revealed an enrichment of inflammatory cells in aged prostates. Together, these findings demonstrated that during normal aging the prostate exhibits phenotypic and molecular characteristics that are also associated with malignancies.					
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INTRODUCTION:

The greatest single risk factor for the development of prostate adenocarcinoma is advanced age¹⁻⁵. Emerging evidence suggests that molecular alterations in the aged prostate microenvironment mediated by stromal aging and senescence are key factors regulating carcinogenesis and neoplastic progression^{6,7}. However, no functional studies have been reported that definitively provide mechanistic evidence of cause and effect. This proposal is designed to investigate the role of the aged-stroma microenvironment in prostate carcinogenesis. Our *hypothesis is that gene expression differences can be identified between normal stroma from young vs. old mice, and that candidate genes identified in the aged-stroma have the potential to influence the proliferation, survival, or invasive capabilities of adjacent transformed epithelium via paracrine mechanisms*. The ultimate goal of this proposal is to provide strong preclinical data that can be translated into novel human studies of prostate cancer prevention.

BODY:

***Task 1.** Identify molecular alterations that occur in the aged prostatic microenvironment that have the potential to influence the proliferation, survival, or invasive capabilities of adjacent transformed epithelium via paracrine mechanisms.*

Effects of age on prostatic cellular composition and morphology

In order to characterize the young and aged mouse prostate, at the cellular and histological level ---prior to any gene expression profile analyses--- we resected the prostate glands from mice of the C57BL/6 strain aged 4-month (n=5; designated young), and 24-month (n=5; designated old) and evaluated by hematoxylin and eosin stain (H&E). We used 4 month-old mice as our young cohort because at this age, they are still young, but sexually mature, and therefore less prone to exhibit changes that are associated with development. After dissection, prostates were fixed, embedded in paraffin, sectioned, and stained with hematoxylin and eosin (H&E) for histological studies. Each prostate lobe was individually compared across age groups. Overall, each prostate lobe showed subtle differences in morphology with aging (representative images are shown in Figure 1). In contrast to young mice, focal atrophy of a small number of acini as well as epithelial atypia coexisted with morphologically normal acini in old mice. The

cellular stroma layer adjacent to the epithelial cells (glandular-adjacent stroma) was generally more disorganized in old animals than in young animals with little evidence of cell orientation and rounding of smooth-muscle/fibroblast cells within the extracellular matrix (Figure 1., brackets and inset). Foci of inflammatory infiltrates comprised of cells with characteristic small cell size and little cytoplasm were observed in the interductal stroma and seemed more abundant in the prostates from old animals (Figure 1, arrows).

To determine the cell composition of the glandular-adjacent stroma we stained prostate sections from young and old mice by double immunofluorescent staining for smooth-muscle-actin and vimentin (a fibroblast cell type marker). We determined that 95% of the adjacent stromal cells stained positive for smooth-muscle actin and only 5% stained positive for vimentin (Figure 2). Thus, the majority of the glandular-adjacent cellular stroma in the mouse prostate is represented by smooth muscle cells, consistent with prior studies of murine and human prostates⁸⁻¹⁰. No significant difference in the ratio of cell types expressing these markers was found between young and old prostates. Of note, there was no overlap between smooth-muscle-actin positive and vimentin positive cells, consistent with the lack of a myofibroblast cell type in normal prostate tissue, in both young and old animals.

Effects of age on gene expression in prostatic stroma

A key objective of this study centered on the analysis of aging-related molecular changes in the stromal compartment of the prostate isolated from its in situ environment. To evaluate the ability of laser-capture microdissection (LCM) to acquire pure cell populations, we performed a pilot study using LCM to separately isolate luminal epithelial cells and glandular-adjacent stroma from young (n=5) and old mice (n=5). We opted to capture cells from the anterior and dorsal lobes since, based on histology, these two lobes have the most abundant cellular smooth-muscle/fibroblastic stroma (Figure 1, brackets). In addition, the anterior and dorsolateral lobes have also been reported to be the regions in which prostate intraepithelial neoplasia (PIN) and prostate carcinogenesis begins in murine models¹¹⁻¹⁵ and gene expression data indicates that the dorsolateral lobe is most homologous to the peripheral zone of the human prostate, where cancer is most prevalent¹⁶. We verified cell-type specific purity by analyzing the expression levels of known stromal cell and epithelial cell markers using a customized mouse prostate cDNA array (MPEDB array)¹⁷. Three biological replicate pools per lobe, representing five 4 month-old and

five 24 month-old animals, were generated to facilitate statistical analyses and control for individual variability. As expected, stromal and epithelial transcripts were differentially expressed in the stroma and epithelial samples respectively (Figure 3B). To further characterize the relationships between the epithelial and stroma samples and between age groups, we performed Principal Component Analysis (PCA) for all the genes in the arrays (Figure 3A). PCA clearly identified a subset of genes that discriminated the epithelial and stroma samples, suggesting that the major differences between samples (53% of the total variance) resulted from the differential expression of large numbers of genes between the stroma and epithelial compartments. These results demonstrate that highly enriched populations of stroma cells can be isolated by microdissection.

We next compared transcript abundance levels in the epithelial and stromal cell compartments and identified 378 and 282 genes to be differentially expressed with aging in the stroma and epithelial samples respectively, as determined by a Student's T-test analysis ($p < 0.05$) (Figure 3 C and D).

In order to test whether the epithelial and stroma compartments showed similar age-related patterns, we performed a Pearson correlation analysis between epithelial and stroma samples using differentially expressed genes ($p < 0.05$), between the young and old prostates for each cell type. The age-related gene expression changes between epithelial and stromal samples showed a low correlation coefficient of 0.3 (Figure 3C and D). This low correlation suggests that prostate tissue aging is not homogeneous in nature, in that different cell types respond to aging differentially, at least at the molecular level. Consistent with this concept, several studies have shown that the pattern of aging/senescent related gene expression is strongly influenced by tissues and/or cell lineage¹⁸⁻²⁰.

To verify the aging-induced gene expression alterations in prostate stroma, we performed an additional microarray experiment from laser captured microdissected adjacent stroma from an independent set of 4 month-old ($n=12$) and 24 month-old ($n=12$) mice and used a microarray platform comprised of oligonucleotides complementary to ~40,000 genes. Using the same t-test cutoff ($p < 0.05$), 718 transcripts were increased and 541 transcripts decreased in aged versus young prostate stroma (Figure 4). A significant correlation coefficient of 0.6 between the two distinct experiments was determined using the most differentially expressed genes ($p < 0.005$). Among the genes significantly up-regulated in the aged prostate stroma that could potentially

influence the proliferation, survival or invasive capabilities of adjacent transformed epithelium are the stress-response molecule Apolipoprotein D (Apod), chemokine (C-C motif) ligand 8 (Ccl8), and the extracellular matrix signaling protein cysteine rich protein 61 (Cyr61/ CCN1). Experiments using qRT-PCR as an independent measurement platform confirmed that Ccl8 and Apod were increased in aged prostate stroma (Figure 5A and 5B, respectively). We confirmed that Apod and Ccl8 are expressed at very low levels in white blood cell isolates and in microdissected epithelium relative to stroma, and no differences were seen between young and old epithelium. Interestingly, the transcripts of both Apod and Ccl8 were also up-regulated in primary mouse prostate smooth-muscle cells and human prostate fibroblasts that were induced to senesce by H₂O₂ exposure or p16 overexpression (Figure 5C for mouse Apod and Ccl8; Figure 5D for human APOD and preliminary results in our laboratory for human CCL8).

Several genes were identified with lower expression in aged relative to young prostate stroma including several genes encoding extracellular matrix proteins Col1a1, Col1a2, Col3a1, among others. We confirmed lower expression levels of these pro-collagen genes by qRT-PCR (see below).

Since histological analysis demonstrated that the aged prostate contains a higher number of inflammatory cells, we were concerned that a component of the aged prostate stroma expression profile could reflect transcripts derived from infiltrating leukocytes. We generated expression profiles from purified white blood cells (WBC) and compared the expression levels of each age-associated stromal gene with abundance levels in the WBC preparation (Figure 6). When multiple test correction was applied to the aging data set and given a moderate estimate of false positive differences (FDR) of 10%, we found that 47% of the genes from our aging stroma expression profile overlap with that of the white blood cell profile (Figure 6B). These results suggest that a large component of the age-associated gene expression changes reflect infiltrating cells, but that substantial changes are also intrinsic to the aging process of the smooth-muscle/fibroblastic stroma and not from differences in cell type numbers (See Figure 6A and Table 1 for final list).

Prostate aging influences alterations in specific molecular pathways

To determine if the age-induced gene expression alterations comprised specific biological programs, we used gene set enrichment analysis (GSEA) to determine the statistical enrichment

of predetermined gene cohorts. We used the Gene Ontology (GO) set (C5) and curated gene sets (C2) which included canonical pathways, and a senescence-associated gene list generated based on human prostate fibroblasts senescent profiles⁶. We found 164 GO gene sets to be significantly enriched in the aged stroma (FDR<25%). These included enrichment of ‘Inflammatory Response’ and ‘Cytokine/Chemokine Activity’ categories (NOM P-value <0.05; FDR <2%). Genes involved in the ‘NF-κB Cascade’ were also enriched in the aged stroma (NOM P-value <0.05; FDR <25%), consistent with prior studies linking intracellular regulation of immune responses in both aging and age-related diseases²¹. GSEA also determined that the category of ‘collagen binding and collagen genes’ was significantly enriched for genes downregulated in aged stroma (NOM p-value<0.05 FDR <25%). Additionally, using the database of curated gene sets, we found that gene sets derived from mouse aged neocortex, cerebellum, kidney and retina were enriched as well as the senescence-associated gene list derived from senescent prostate fibroblasts (NOM p-value <0.05 FDR <25%). Consistent with these results, analyses of the aged rat prostate^{2,3} as well as studies using different tissues and species---including mice and humans²²--- identified greater expression of inflammatory and stress-response genes, along with a decrease in extracellular matrix components with age, suggesting a common pathway(s) that regulates aging²²⁻²⁴. However, these analyses could not determine which cellular compartment contributed to the expression changes, as they were performed using whole prostate lobes or tissues. In contrast, our study clearly demonstrated that genes up-regulated in the aged prostate stroma, such as *Apod* and *Ccl8* were specifically associated with the stroma compartment and not the aged epithelium.

Increased immune cell infiltration of prostatic tissue with advanced age

The microarray data analysis comparing changes in the prostate stroma with aging suggests that the aged prostate presents a pro-inflammatory environment in the aged animals, with the induction of pro-inflammatory chemokines such as *Ccl8* and *Ccl12*, among others. Increased expression of these genes strongly suggested that the stroma cells in the older animals were responding to inflammatory signals. Since the up-regulated chemokines are potent chemoattractants for T cells, macrophages, natural killer (NK) cells and B cells, we then wanted to determine the composition of the immune cell population. Therefore, to begin characterizing the type and location of these inflammatory cells present in the aged prostate, we stained prostate

tissues from aged (n=10) and young (n=10) animals for several markers that specify inflammatory cell types: F4/80 (macrophages), CD3 (T cells) and B220 (B cells). Figure 7A-F illustrates the staining of immune infiltrates in the old and young anterior prostate for the various immune cell markers and demonstrates that the number of B cells, T cells and macrophages were significantly increased in the aged prostate (B-cells $p=0.0496$; T-cell $p=0.0030$; Macrophages $p=0.0008$; Figure 7G). We then evaluated the localization of these immune cells and determined the number of cells positive for each immune cell marker. Inflammatory infiltrates were divided into three different categories: periglandular stromal infiltrates (inflammatory cells in contact with the smooth-muscle/fibroblastic cellular stroma); intraglandular infiltrates (inflammatory cells in contact with the glandular luminal epithelium); and interglandular infiltrates (inflammatory cells in the interglandular space). The number of macrophages and T cells in contact with the luminal epithelium (intraglandular), with the cellular smooth-muscle stroma (periglandular) and in the space between glands (interglandular) were significantly higher in aged prostates compared to young prostates ($p<0.05$) (Figure 7G). There was a low number of B cells in contact with the epithelium and smooth-muscle cells (range from 1-16 cells per 10x field, and most of the cases B cells were absent) in both young and aged mice. However, in the interglandular space, B cells were present in a significantly higher number in the aged prostate compared to young prostates ($p=0.0530$) (Figure 7G). Although we did not stain the prostate gland for NK cells, higher gene expression of NK specific markers (Nkr-P1C, Nkr-P1A and Cd49b) were also found in the prostate tissue of the aged mice ($p<0.05$; Figure 7H). These observations, along with the increased expression of immune-specific genes (especially chemokines and immunoglobulin genes) are consistent with the increased infiltration of lymphocytes and macrophages in the aged mouse prostate.

The elevated numbers of inflammatory cells in the aged prostate prompted us to investigate the potential reasons for this finding. By H&E staining of 10 prostate tissues from each age group, we were able to discard the possibility of an inflammatory response due to bacterial infections, since neither obvious bacteria infection nor the associated neutrophilic infiltrates were present in the mouse prostates from young or old animals. Thus, one reason for the presence of the inflammatory cells in the aged prostate might be a consequence of increased levels of chemokines/cytokines originating from the aged smooth-muscle fibroblastic stroma. However, we cannot rule out the possibility that the increase in transcript levels of these

cytokines, at least for Ccl7 and Ccl5 is due to the presence of infiltrating inflammatory cells in the stromal samples (Figure 6B). To date we have not been able to demonstrate whether the increased levels of chemokines, such as Ccl8 in aged prostate originate from smooth-muscle/fibroblastic cellular compartment, the inflammatory cells, or both. However, the fact that Ccl8 and Apod were not expressed in the white blood cells isolated from young and old C57BL/6 mice, suggests that these alterations are likely to be intrinsic to the microdissected glandular associated stroma enriched in smooth muscle cells and fibroblasts. Alternatively, genotoxic/oxidative stress and changes in the extracellular matrix could also induce the infiltration of inflammatory cells observed in the aged prostate.

A link between genotoxic stress and the activation of the innate immune system through NF- κ B activation has been proposed as a cause of premature aging, via “inflamm-aging” processes ²¹. Our observation on the age-related induction of genes that respond to genotoxic/oxidative stress (such as Apod, and Serpinb5), and those involving the NF- κ B pathway (such as Stat1 and Tlr1), suggest that cumulative stresses associated with the normal process of aging (e.g., oxidative stress and extracellular matrix alterations) could evoke an inflammatory response possibly through the activation of the NF- κ B pathway ²¹. Taken together, our data suggest that intrinsic and extrinsic events associated with aging act in concert to promote a proinflammatory tissue microenvironment.

Chronic inflammation has emerged as a potential risk factor for carcinomas in many organs such as the liver, colon, bladder, lung and pancreas ²⁵. Although, conflicting data exist regarding the causal effect of chronic inflammation with prostate cancer, there is a significant volume of compelling evidence supporting a role for inflammation in the pathogenesis of prostate cancer ²⁶⁻²⁸. Thus, our observation demonstrating an inflamed prostate in aged animals with an increasing numbers of immune cells, suggests that aging correlates with a pro-inflammatory state which in turn may well influence prostate neoplasia.

Effects of aging on prostate extracellular matrix components and tissue architecture

The transcript profiling studies determined that genes encoding structural extracellular matrix components were expressed at lower levels in aged relative to young prostate stroma. These included several collagen-encoding genes; collagen I α 1 and α 2 subunits, and collagen III α 1 subunit. We confirmed significantly lower transcript levels of Col1a1, Col1a2, Col3a1 and

Col4a1 in aged stroma by qRT-PCR (Figure 8A). To further investigate these findings, we used fluorescence and ultrastructural microscopic analysis to determine the relationship between collagen structure and aging. Examination of the extracellular matrix (ECM) surrounding prostate epithelial cells by immunofluorescent staining for Collagen Type I demonstrated that the majority of the stroma around the prostatic ductal structure is fibrillar collagen (Figure 8C and 8D). Interestingly, although immunofluorescence detection for Type-I collagen did not show substantial differences at the protein level between young and old prostate tissue, it revealed a disorganized collagen matrix network with a coarse and fragmented appearance and less regular distribution of the collagen fibrils in prostates from old animals compared to the fine collagen fibrils and highly organized network in prostates from young animals (Figure 8C and 8D, respectively). In order to rule out that the disorganization of the collagen fibers was due to mechanical damaging during sectioning, 30µm sections of the anterior prostate lobe were stained by immunofluorescence with Collagen Type I and were evaluated by confocal microscopy in order to obtain a stack of images inside the intact tissue. Six scoring criteria were used to quantify the differences in collagen fiber appearance (organized, compact, sharp, disorganized, swollen and fuzzy collagen fibers). Five young and five old anterior prostates from independent mice were used and 4 images were taken from each sample (2 images were taken randomly from the tip of a duct and 2 on the side). Images were independently scored by three individuals (including one pathologist). Collagen fibril appearance was significantly different between young and old prostates, demonstrating that more than 70% of the old prostates evaluated have a disorganized, swollen and fuzzy fibers ($p<0.05$) compared to the organized, compact and sharp collagen fibril appearance from young mice ($p<0.005$) (Figure 8B). Similar alterations were observed in sections from the dorsal, lateral and ventral lobes; however, to quantify the observations, the wider stroma layer in the anterior lobe was chosen to facilitate the scoring.

To investigate in greater detail the structural alterations of the collagen network in the aged prostate, we performed scanning electron microscopy using prostates from young ($n=5$) and old ($n=5$) animals. To visualize the three-dimensional organization of the collagenous stroma, samples were treated with serial washes of 10% NaOH solution to remove all cellular elements^{29,30}. The acellular preparations (Figures 8E and 8F) showed that a smooth and grossly homogeneous fibrous network lines the empty acinar space. Due to difficulties imaging the internal ducts of the acinar it was not possible to assess whether this surface exhibits differences

between young and old prostates. However, on the outside of the ducts, a spongy-like organization was apparent. The young prostates displayed a meshwork of loosely woven fibrils comprised of distinct collagen bundles, while in aged mice collagen bundles were adherent or joined to each other (Figures 8 E'-E'' and 8 F'-F'', respectively). These observations were similar to that seen by the immunofluorescence staining for Collagen Type I (Figure 8C and 8D). Collectively, the collagenous stroma in aged mouse prostate is characterized by a disorganized and disrupted collagen matrix. To our knowledge, this is the first study that demonstrates alterations in the collagen network with aging in prostate tissue.

To further characterize the aged mouse prostate at the ultrastructural level, we performed transmission electron microscopy (TEM) analysis in young (n=4) and old (n=4) mouse prostates (Figure 9A and 9B, respectively). In agreement with the immunofluorescence analysis for Collagen Type I, we found that despite the lower levels of procollagen I alpha-1 mRNA in the aged animals, they also exhibited a dramatic increase in collagen fibers in the stroma as determined by TEM (compared Figure 9 B and 9D, brace). Additionally, since we demonstrated that the basement-membrane-codifying pro-collagen Col4a1 mRNA was down-regulated with aging (Figure 8A), we then analyzed the organization of the basement membrane by TEM in young and aged prostate. Although we did not find any obvious structural alterations or disruptions in the basement membrane between age groups, we did observe epithelial cytoplasmic projections extending towards the extracellular matrix in the aged prostate (Figure 9B', yellow square), indicating that the aged basement membrane is less rigid, thus allowing these epithelial cells to compress it towards the extracellular matrix. This observation highlights the potential effect of an aged microenvironment permissive for malignant cells to invade. Consistent with these findings, similar ultra-structural phenotypes have recently been observed in the aged Mongolian gerbil ventral prostate³¹. In addition to the collagenous matrix, we also wanted to determine whether the cells (mainly smooth muscle cells) within the altered extracellular matrix presented proper organization. In aged prostates, the smooth muscle cells presented a less consistent orientation within the stroma and did not have a continuous parallel arrangement as observed in young prostate (Figure 9B-B', asterisk, and 9A-A', respectively).

It is well established that TGF- β plays a central role in regulating collagen homeostasis, since it both stimulates collagen synthesis and down-regulates expression of collagen-degrading

MMPs³²⁻³⁷. In the present study, based on the microarray data, we did not find any alterations in gene expression in either TGF- β or its receptors, but further analyses need to be performed using qRT-PCT and/or IHC to confirm these results. However, interestingly, Cyr61 was highly up-regulated in the aged stroma and it has been identified as a pivotal regulator of collagen production and degradation in aged and photo-aged human skin³⁸. Elevated CYR61 in human skin fibroblasts down-regulates TGF- β type II receptor, thus impairing the TGF- β pathway, and induces the expression of MMP-1 and a subsequent fragmentation of collagen³⁸. Thus, it is possible that the down-regulation and alterations of the collagen matrix observed in the aged mouse prostate could well be due to the high expression of Cyr61. Of note, a mouse model where TGF- β type II receptor is inactivated in fibroblasts resulted in intraepithelial neoplasia (PIN) in the prostate and invasive cancers of the forestomach³⁹. Taken together, the over-expression of Cyr61 might link carcinogenesis through inactivation of TGF β RII and subsequent alterations of the ECM which could further affect tumor progression and spread.

Our observation that the collagenous stroma in the aged prostate is highly disorganized, partially fragmented and with a tendency of the collagen bundles to adhere with each other (as demonstrated by immunofluorescence and scanning electron microscopy), together with our finding that the aged prostates had the greatest amount of collagen fibers (as detected by TEM), suggests that the age-related collagen alterations may be a consequence of age-associated changes of collagen cross-linking⁴⁰⁻⁴² and impairment of its degradation⁴³ rendering an accumulation of partially degraded fibrils⁴⁴. Collagen fragmentation has been shown to promote oxidative stress⁴⁴, consequently, alteration of the ECM with aging could also explain the increased expression of stress response genes, such as Apod and Serpinb5, as well as the increase in inflammatory infiltrates in the aged prostate.

Task 2. *Determine the functional role of specific aging-related paracrine-acting stromal factors through the development and analysis of in vitro and in vivo co-culture systems modeling aged-stroma and prostate cancer.*

Effect of Ccl8 and ApoD on mouse prostate tumor cell growth

To determine the effect of ApoD and Ccl8, (candidate factors identified in task 1) on the proliferation of mouse prostate cancer cell lines (e.g., TRAMP C2 and MycCaP), I attempted to clone the Ccl8 and ApoD genes. However, the cloning strategies employed were not successful for either gene. As an alternative approach to evaluate the specific effect of CCL8 and APOD on prostate epithelial cell growth, I used recombinant CCL8 and APOD. Mouse TRAMP C2 and MycCaP tumor cells were seeded in DMEM + 5% FBS containing increasing concentrations of recombinant CCL8 or APOD (0, 10, 20, 100 ng/ml). The cultures were incubated for 24 hours and viable cell numbers were determined by the colorimetric MTS assay (Figure 10). The addition of recombinant CCL8 or APOD (10-100 ng/ml) did not induce the proliferation of TRAMP C2 or MycCaP relative to the cells grown in the absence of CCL8 or APOD. Thus, at least in the conditions tested, recombinant ApoD and Ccl8 did not have any affect on the growth of mouse prostate tumors cells, however I cannot rule out that in different culture conditions (absence of serum in the media, addition of other growth factors) I could observe a significant effect of these proteins on the proliferation or migration of prostate benign or malignant epithelial cells⁴⁵⁻⁴⁷.

Effect of the aged collagen matrix on the proliferation and invasive capabilities of prostate cancer cells

To begin to address the functional relevance of the age-dependent effect of collagen on tumor growth and invasiveness of prostate epithelial cells, in vitro 3D collagen gels were created by extracting mouse tail tendon collagen from young (4 month-old) and old (20-24 month-old) C57BL/6 mice. In collaboration with Dr. May Reed at the Harborview Medical Center, we have shown that tail tendon collagen extracted from young and old mice exhibit changes in the rates of collagen fibril formation, fibril size and density, and adherent fibroblast function⁴⁸ (Figure 11). These studies demonstrated that some of the changes observed in aged collagen matrix in vivo

can be modeled in vitro, providing support for the use of young and old 3D collagen gels to analyze age-related cellular-matrix interactions

To determine whether and to what extent tumor cells could invade young and old collagen gels, we used the trans-well cell culture assay. Mouse prostate cancer cell lines (TRAMP-C2 and Myc-CaP) were seeded on top of polymerized young and old collagen inserts, placed in invasion chambers, and allowed to invade for 18 hrs. Invaded cells were counted by fluorescence microscopy in random fields. The number of cells that invaded through the aged collagen was significantly higher than in the young collagen at similar concentrations ($p=0.07$ for TRAMP-C2 and $p=0.0016$ for Myc-CaP (Figure 12). In fact, for the concentration of collagen used (0.6 mg/ml), very few cells invaded through young collagen. These findings suggest that alterations that occur with aging in the collagenous material of the extracellular matrix may present an inductive and/or permissive environment for tumor cell invasion. Since it has recently been shown that the rigidity of the extracellular matrix can regulate tumor cell growth, both in vitro and in vivo, we then analyzed the proliferation of prostate epithelia cells when plated on top or within the 3D young and aged collagen gels for 24 hours. TRAMP-C2 and Myc-CaP cell lines grew at a slightly higher rate in old collagen, however the growth difference between young and old collagen was not statistically significant (Figure 13). Since fibroblast cells are known to respond to alterations in the collagen network and furthermore, to induce changes in gene expression, including integrins and soluble factors, we next determined if the growth of epithelial cells could be induced by paracrine factors secreted by resident fibroblasts in response to the aged-collagen microenvironment. Similarly, we did not observe differences in proliferation when these cells were cultured in the presence of 3T3 fibroblastic cells in young and old collagen (Figure 13).

In this study, we provide evidence that biologically aged collagen promotes (or allows) the invasive migration of prostate cancer cells in vitro. Our data supports the idea that age-related ECM alterations could be implicated in the progression and metastasis of malignant cells^{49,50}. However, it remains to be determined whether structural or signaling properties of the aged collagen were responsible for the increase invasion of tumor cells.

Increasing evidence supports the potential implications of the collagen content, fiber structure, and organization, as key determinants of tumor cell behavior. In vitro studies demonstrated the effect of fibrillar collagen and substrate rigidity on epithelial cell proliferation,

apoptosis, and motility, which suggests a direct role of the collagen network on the behavior of epithelial cells⁵¹⁻⁵⁴. Moreover, recent in vivo studies demonstrated that higher collagen density increased tumorigenesis, local invasion, and metastasis of mammary epithelial cells, causally linking an increase in stromal collagen to tumor formation and progression⁵⁵. In the prostate, it has been shown that collagen type IV enhances the growth of rat ventral prostatic epithelial cells in vitro⁵⁶, and that type I collagen mediates proliferative responses of PC3 prostate carcinoma cells⁵⁷.

Taken together, we hypothesize that the disorganized collagen matrix and the diminished expression of pro-collagen genes in the aged prostate microenvironment may have an effect on the structural and signaling properties of the extracellular matrix. In turn, a dysfunctional ECM in the aged prostate could plausibly facilitate carcinogenesis and neoplastic progression. Furthermore, an altered ECM could also create an inflammatory environment which in turn could promote carcinogenesis.

***Task 3.** Determine the concordant findings between murine aging-related stromal changes and human stromal alterations associated with senescence and neoplastic progression, in order to identify the aged-related stromal factors most likely to be of relevance in human prostatic carcinogenesis*

Correlations between in vivo aging and in vitro senescence

Although the molecular process of replicative senescence is intimately associated with features of aging, it has been challenging to directly determine whether senescent cellular phenotypes normally accumulate with aging in numbers sufficient to influence pathological processes in vivo. We selected several genes known to be associated with in vitro senescence and compared their transcript levels between young and aged prostate stroma. The first cohort we evaluated were those comprising a senescence-associated secretory phenotype (SASP) shown to directly influence epithelial cell growth⁶. Unexpectedly, none of the senescence associated candidate factors we evaluated, Hgf, Ctgf, Fgf7, Cxcl12, Areg, Il6, Il1a, Cxcl1 and Gm-csf, were up-regulated in the aged mouse prostate stroma (Figure14A, for genes whose transcripts were detectable in microdissected stroma). However, several transcripts we determined to be elevated

in aged stroma in vivo, such as *Apod* and *Ccl8*, were significantly increased in senescent versus pre-senescent prostate smooth-muscle cells and fibroblasts in vitro (Figure 5 C and D).

Employing a more systematic approach, we compared the transcriptional profile of aged murine stroma measured in this study (considering a false discovery rate (FDR) <25% and including those transcripts also found in WBC), with previously determined transcriptional profiles of human prostate fibroblasts induced to senesce by different means (H_2O_2 , Bleomycin, replicative senescence and overexpression of p16 and oncogenic RAS ⁶ and unpublished data). Of 264 genes significantly altered in aged mouse stroma, 37 genes were also significantly altered in at least one senescence profile (FDR<25%). Genes involved in the NF- κ B pathway, such as *STAT1* and *TLR1*; cell proliferation/apoptosis, such as *IER3*; *EHF*; *LRPAP1* and inflammation such as *CCL7*; *CXCL16*; *B2M*; *IL7R* and *LGALS3* were among the genes whose expressions were altered in both in vivo aging and in vitro senescence. The changes of these gene groups are in agreement with the age-enriched biological functions identified by pathway-based analyses described below.

In order to determine whether the senescent secretory phenotype described in human senescent fibroblasts ⁶ is also present in smooth muscle cells from the mouse prostate, we isolated prostatic smooth muscle cells from 3 young C57BL/6 mice and induced them to senesce by exposure to H_2O_2 . As a first approach, we performed qRT-PCR to evaluate the expression levels of those senescence-associated secretory factors identified in human senescent fibroblasts, including *Hgf*, *Ctgf*, *Fgf7*, *Cxcl12*, *Areg*, *Il6*, *Il1a*, *Cxcl1* and *Gm-csf*. Similar to our studies of young and aged mouse prostate stroma in vivo, the mouse prostate senescent smooth-muscle cells did not exhibit higher expression of these soluble factors with the exception of *Hgf* (Figure 14C). Senescent markers including SA- β -Gal (Figure 11A-B) and up-regulation of p16 (Figure 14C) confirmed the senescent state of these cells. Taken together, these results suggest that a subset of molecules altered in the aged stroma of the mouse prostate, are also present in both human and mouse senescent prostate fibroblast and smooth muscle cells, respectively, though a complete overlap between these cellular states (in vitro senescence and in vivo aging) does not exist.

Considering that inflammatory processes can induce senescence and that senescent cells can secrete inflammatory chemoattractants ^{6,58}, it remains to be determined whether inflammatory infiltrates in the aged prostate induce an age/senescent response, as reflected in

gene expression changes in the smooth muscle cell/fibroblast compartment, or that the aged smooth muscle cell/fibroblast compartment, through the secretion of proinflammatory chemokines such as Ccl8, Ccl12, Ccl5 and Ccl7, contributes to the tissue inflammatory state observed in the aged prostate.

Task 4. Write initial manuscript (Months 31-34)

Manuscript in press. PLoS ONE 2010. Sep 01.

KEY RESEARCH ACCOMPLISHMENT:

- We have identified an age-associated gene expression profile of the mouse prostate stroma isolated from its *in situ* environment.
- We have confirmed that factors identified in this study, such as Apod and Ccl8, were selectively expressed and up-regulated only in the aged prostate stroma and not in the prostatic epithelium or inflammatory cells.
- We have demonstrated that the prostate microenvironment from aged mice is characterized by a pro-inflammatory state with up-regulation of inflammatory chemokine genes and a high number of inflammatory cells.
- We have demonstrated that the extracellular collagenous stroma in aged prostate presents a disorganized and disrupted collagen matrix.
- We have demonstrated that biologically aged collagen promotes (or allows) the invasive migration of prostate cancer cells *in vitro*.
- We have demonstrated that the molecular phenotype of *in vivo* aged stroma does not present a complete correlation with the senescence-associated secretory phenotype described in human senescent fibroblasts *in vitro*. Only a subset of molecules altered during *in vivo* aging are also altered in *in vitro* senescence, both in human and mouse cells.

REPORTABLE OUTCOMES:

Poster presentation:

Poster title: “Expression Profiles of the Aged Prostate Microenvironment Identify Alterations in Transcripts Encoding Extracellular Matrix Proteins: Implications for Prostate Carcinogenesis” Presented at the Translational Research at the Aging and Cancer Interface (AACR) February 20-23, 2007.

Talk:

“Studies of Normal Variation and the Aged Microenvironment in the Prostate: Implications for Prostate Cancer”. FHCRC. December 10th, 2009. Seattle, WA.

Manuscript:

1. **Daniella Bianchi-Frias**, Funda Vakar-Lopez, Ilsa M Coleman, May Reed, Steven S Plymate, and Peter S. Nelson. The Effects of Aging on the Molecular and Cellular Composition of the Prostate Microenvironment. PLoS ONE. 2010 Sep 01 (in press)

CONCLUSION:

We identified significant changes in the structural composition, inflammatory cell populations, and intrinsic cellular gene expression of resident stroma cells. This study generated four main conclusions: First, aging-related changes in gene expression are cell type-specific. Second, the aged stroma expresses factors involved in oxidative/environmental stress responses, such as Apod, Serpinb5, and soluble factors previously involved in the pathogenesis of prostate cancer, such as Cyr61 and NF- κ B target genes. Third, there is a pro-inflammatory state in the aged prostate with an increased expression of inflammatory chemokines and infiltrating cells. Fourth, the collagen matrix is significantly disrupted in the aged prostate and collagen extracted from aged-mice tail tendons induced (or allowed) the invasive migration of prostate tumor cells. We propose that a subset of the aging-associated changes is causally involved in the development or progression of prostate carcinoma.

Together, our findings provide clues to age-associated molecular events that may be causally-related to alterations in prostate function and that could contribute to the high incidence

of prostate cancer in the aged population. It is plausible that both the alteration in the collagenous stroma and the infiltration of inflammatory cells act in concert with one another to produce fundamental changes in both the prostate epithelial and stromal cells that can lead to prostate tumorigenesis and progression.

In sum, this work provides novel data regarding age/senescence-associated candidate genes important in prostate carcinogenesis. We anticipate that the structural and molecular alterations in the aged prostate identified in this study will provide strong preclinical data that can be translated into novel human studies of prostate cancer prevention and improved treatment in geriatric oncology.

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Appendices

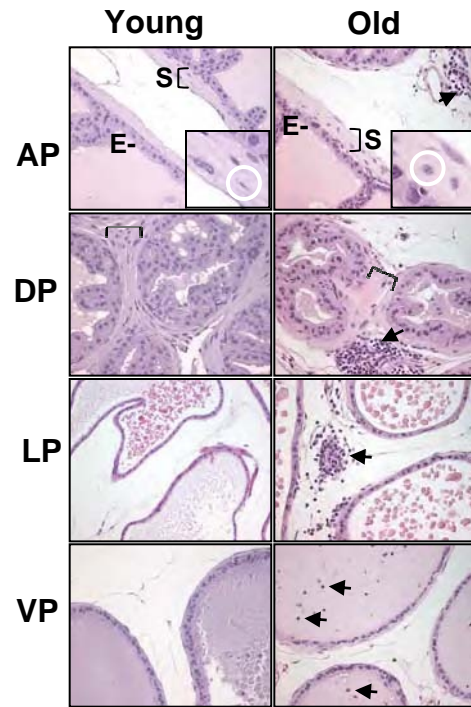


Figure 1. Histological features of prostates from young and old mice as observed in 4-um hematoxylin and eosin-stained sections from formalin-fixed tissue. E: Luminal epithelium; S: Stroma adjacent to the epithelial cells. Note the thick glandular-adjacent cellular stroma (S, bracket) observed in dorsal and anterior lobe. AP insert: smooth-muscle cells (circled in white) appear less stretched and more rounded in the aged prostate with little evidence of cell orientation. H&E revealed frequent areas of inflammatory cell infiltration in the prostates of old animals (arrows). AP: anterior prostate; DP: dorsal prostate; LP: lateral prostate and VP: ventral prostate. (Magnification: 20x).

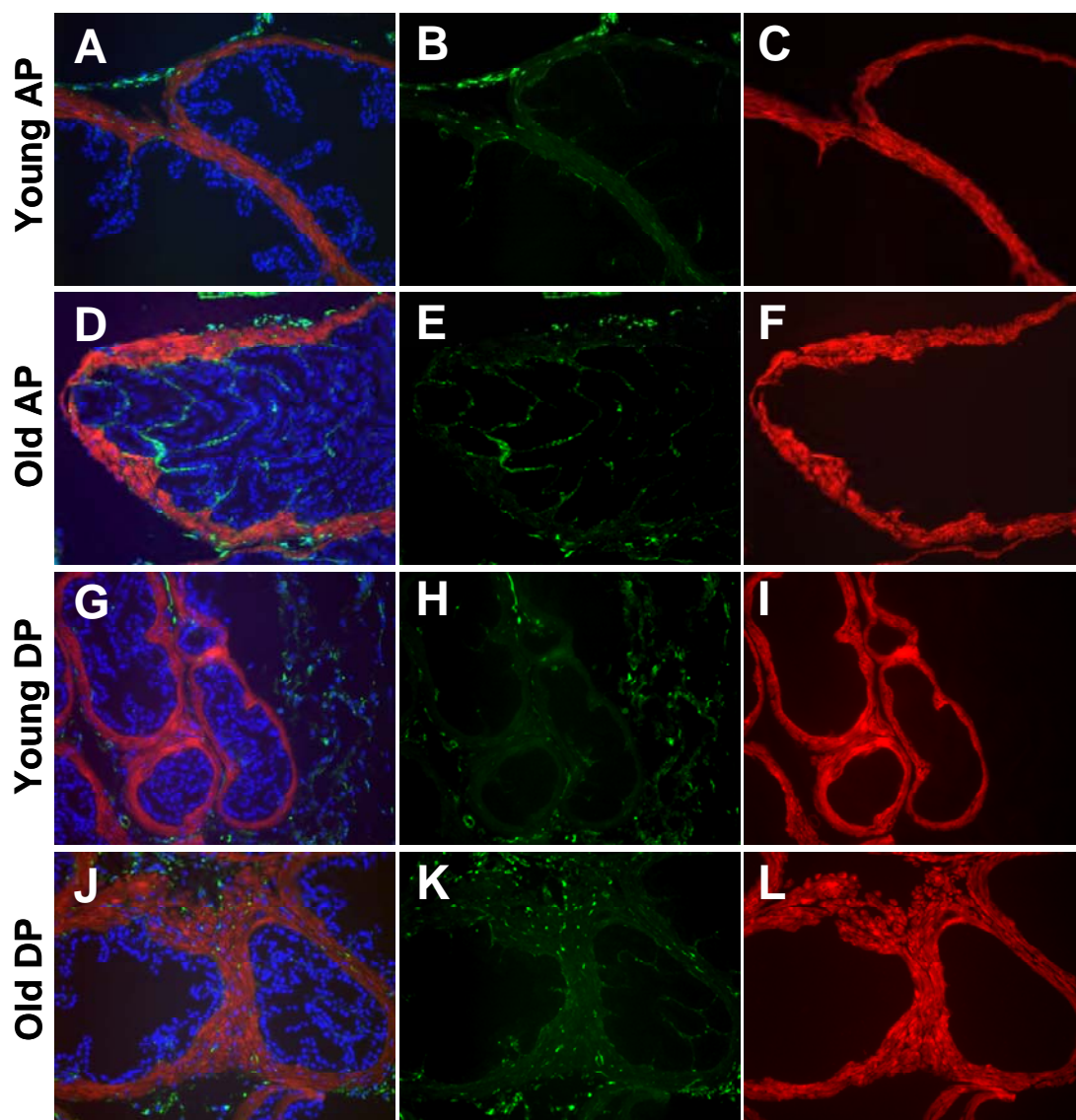


Figure 2. The majority of the prostatic glandular-adjacent stroma is composed of smooth-muscle cells. Double immunofluorescent stain for smooth-muscle-actin (Red; C, F, I and L) and vimentin (green, B, E, H and K) demonstrating the prevalence of smooth-muscle cells (in red) in the glandular-adjacent stroma in both young (A,C,G, I) and old (J, L, D, F) prostates. Scatter fibroblast (in green) are also present in the glandular-adjacent stroma. A, D, G and J are merged images (Blue: DAPI, Red: smooth-muscle-actin, Green: vimentin).

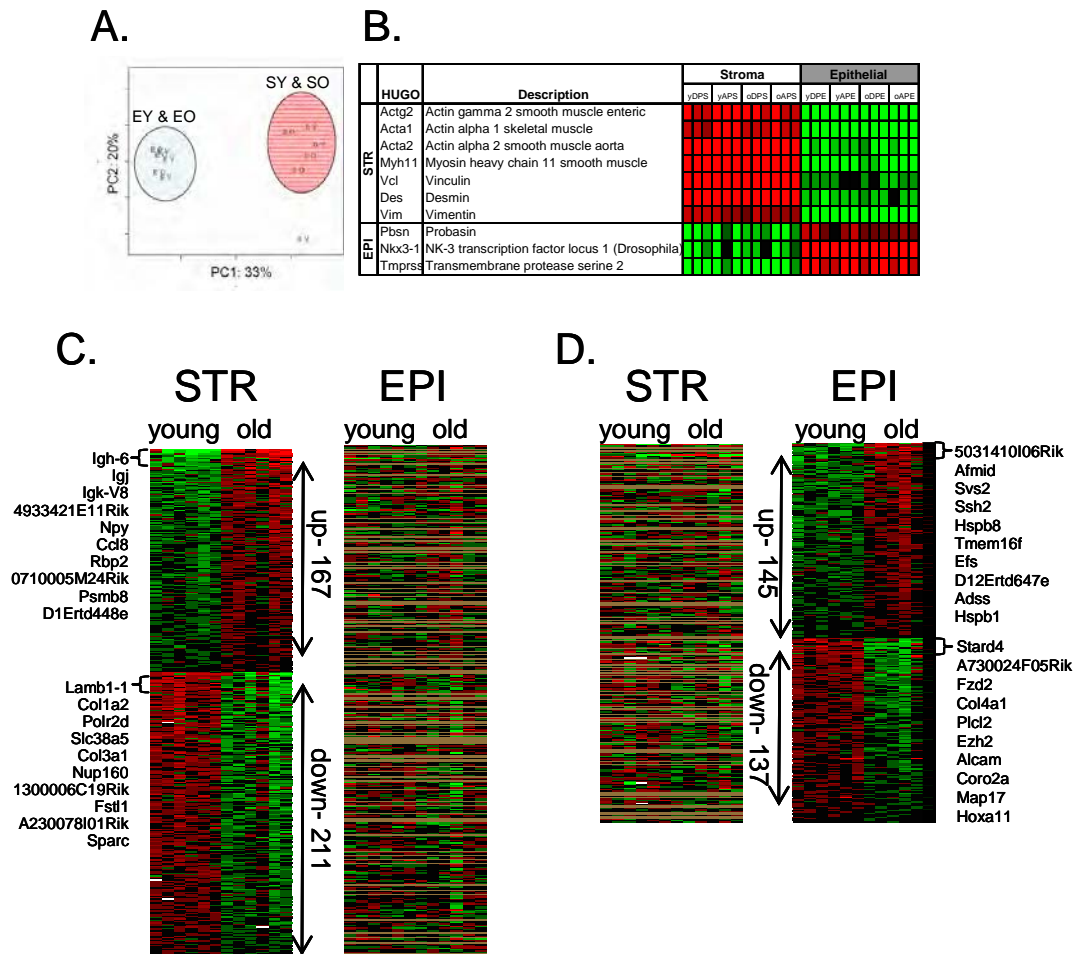


Figure 3. Age-associated transcriptional profile of the mouse prostate is cell-type specific.

A) Principal Component Analysis (PCA) for dorsal prostate stroma and epithelial microdissected samples from young and old animals. PCA clearly identified a subset of genes that discriminated the epithelial and stromal samples. **EO**: old epithelium; **EY**: young epithelium; **SO**: old stroma; **SY**: young stroma. **B)** Transcript abundance levels (Log2 Ratios) obtained from MPEDB arrays of known stromal and epithelial markers, showing that stromal and epithelial transcripts were differentially expressed in the stroma and epithelial microdissected samples respectively, corroborating that highly enriched populations of stroma cells can be isolated by microdissection. Red indicates increased expression; green indicates decreased expression. **C)** Heat map of significantly age-associated transcripts in the prostate stroma ($p < 0.05$) compared to epithelium. Insert: Gene symbols for the 10 most up- and down-regulated genes in the aged stroma. **D)** Heat map of significantly age-associated transcripts in the prostate epithelium ($p < 0.05$) compared to stroma. Insert: Gene symbols for the 10 most up- and down-regulated genes in the aged epithelium. Note the low correlation between the age-related profile of the stroma compared to the epithelium and vice-versa. (C,D) Heat map colors reflect fold ratio values between sample and reference pool and mean-centered across samples. Columns represent biological replicates from dorsal and anterior microdissected epithelium and stroma for each age group. Rows represent individual genes. Values shown in red are relatively larger than the overall mean; values shown in green are relatively smaller than the overall mean. **STR**: microdissected glandular-adjacent stroma; **EPI**: microdissected luminal epithelium.

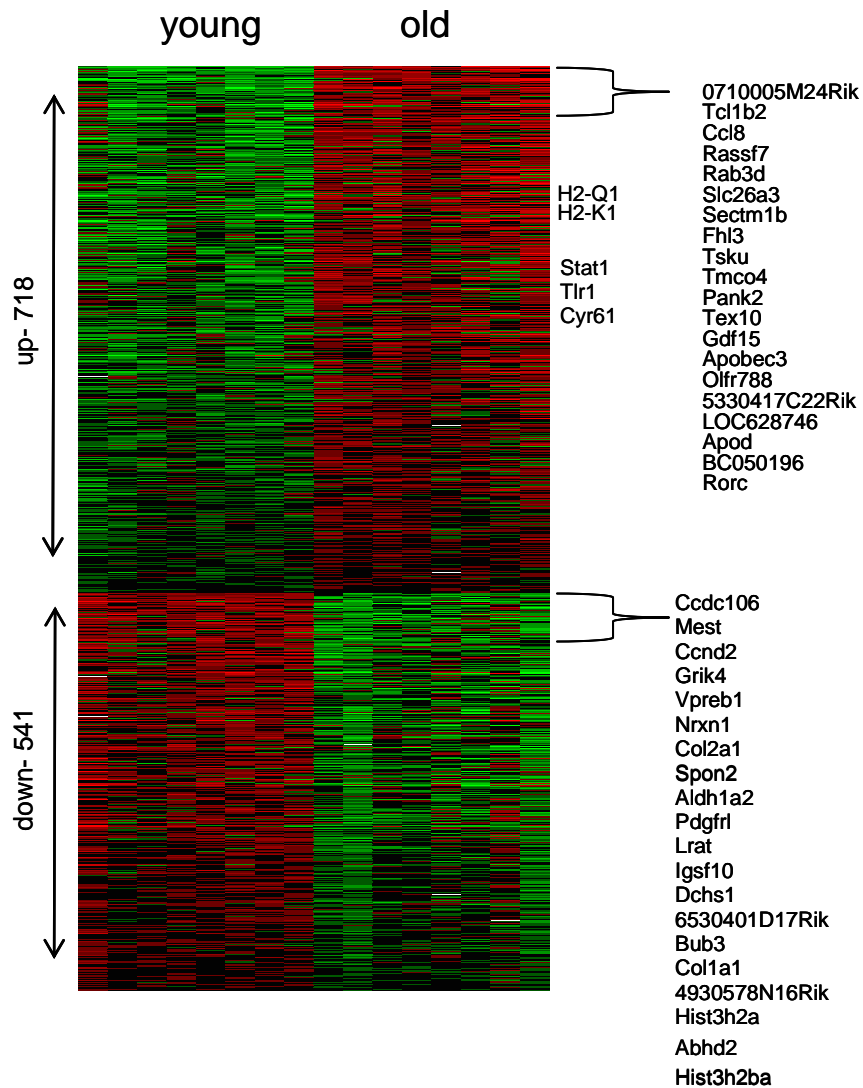


Figure.4. Stromal age-associated transcripts. Heat map for the most differentially regulated genes ($p < 0.05$) from microdissected glandular-adjacent stroma, using an independent set of 4 month-old ($n=12$) and 24 month-old ($n=12$) C57BL/6 mice and a microarray platform comprised of oligonucleotides complementary to ~40,000 genes (44K microarray, Agilent). Gene symbols shown are the top 20 most up and down-regulated genes, other genes of interest are next to the heat map. Heat map colors reflect fold ratio values between sample and reference pool and mean-centered across samples. Columns represent biological replicates from dorsal and anterior microdissected stroma for each age group. Rows represent individual genes. Values shown in red are relatively larger than the overall mean; values shown in green are relatively smaller than the overall mean. Un-paired, two-sample t-test was used to identify significant genes. $p < 0.05$ was considered significant.

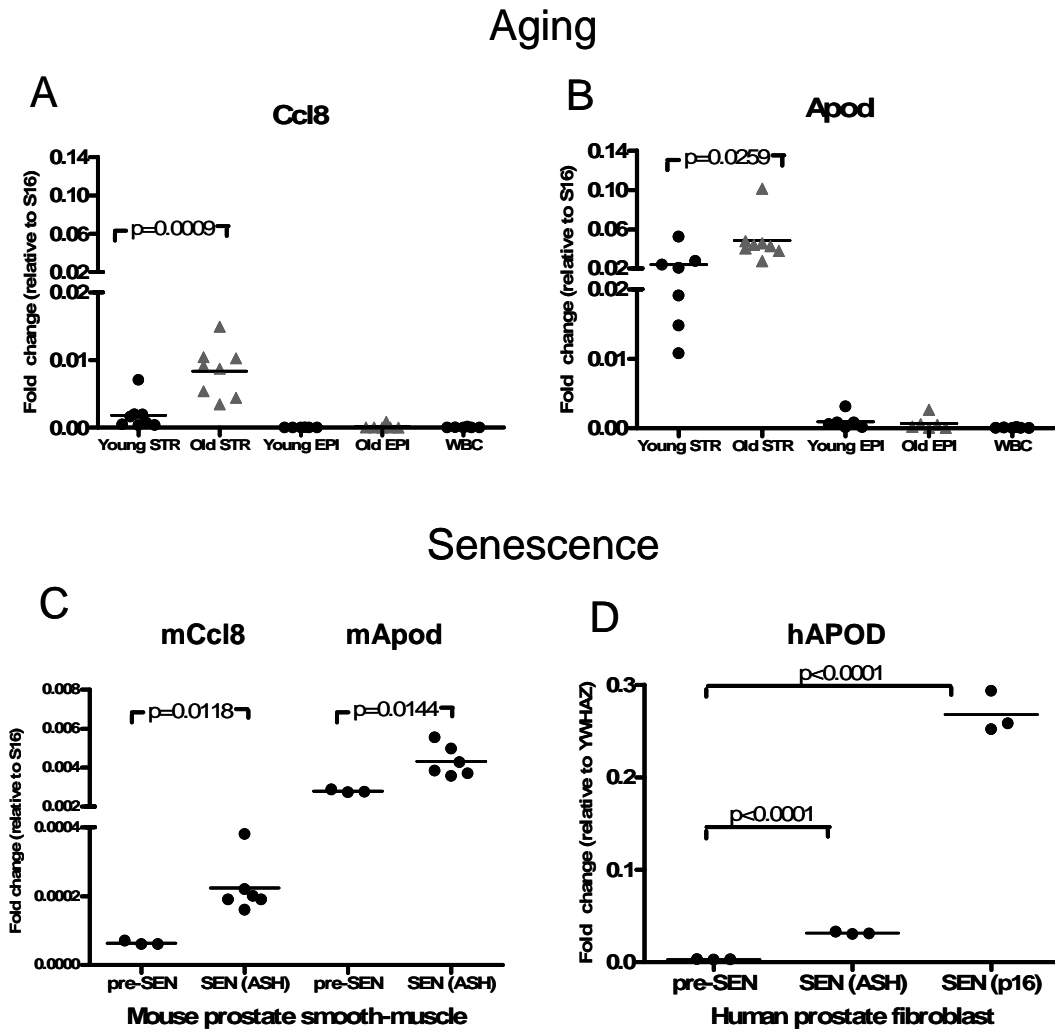
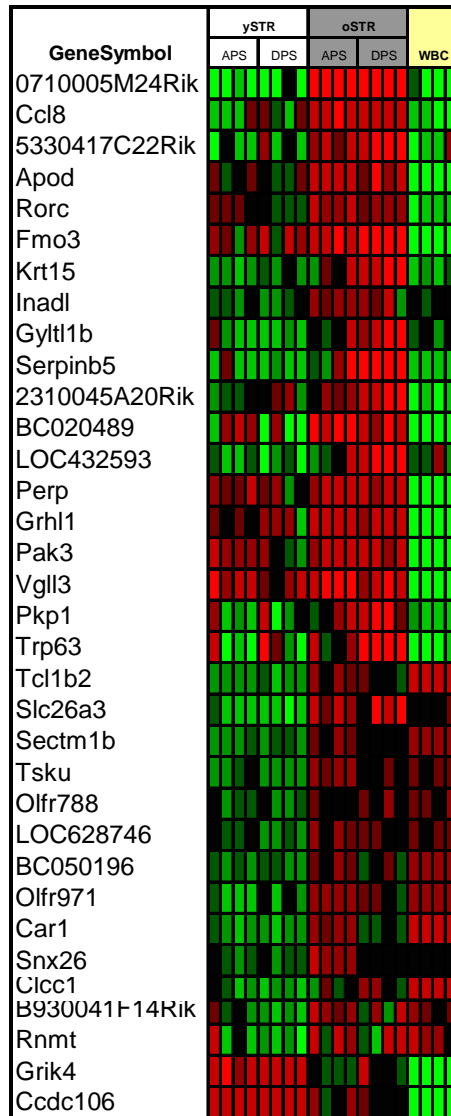


Figure 5. Stroma specific up-regulation of Ccl8 and Apod with aging and senescence.

A,B) Confirmation of stromal age-related changes in gene expression by qRT-PCR. RNAs were reverse transcribed and amplified using qRT-PCR with primers specific for Ccl8 and Apod. RNAs used were as follow: microdissected glandular-adjacent stroma (STR) and epithelium (EPI) from dorsal (n=4) and anterior (n=4) prostate lobes from C57BL/6 young (n=14) and old (n=14) mice used in microarray analyses. White blood cells (WBC) were isolated from young and old C57BL/6 mice (n=6). Note the higher expression of Ccl8 and Apod in the microdissected old stroma (Old STR) compared to young stroma (young STR). Also notice the low abundance in transcript levels of these two genes in microdissected young and old epithelium (Young EPI, Old EPI, respectively) and in white-blood cells (WBC). **C,D)** Genes identified to be altered in vivo in the aged stroma were also found to be up-regulated in mouse and human prostate stromal cells. **C)** Mouse pre- and senescent prostate smooth muscle cells isolated from 3 young C57BL/6 mice. Pre-SEN: pre-senescent cells; SEN (ASH) cell induced to senesce by H₂O₂ exposure. Ribosomal S16 transcript expression levels were used to normalize mouse qRT-PCR data. **D)** Human pre- and senescent prostate PSC31 fibroblasts. Pre-SEN: pre-senescent cells; SEN (ASH) cell induced to senesce by H₂O₂ exposure; SEN (p16) cell induced to senesce by over expressing p16. YWHAZ transcript expression levels were used to normalize the human qRT-PCR data.

A. Intrinsic aged stroma profile



B. High transcript abundance in WBC

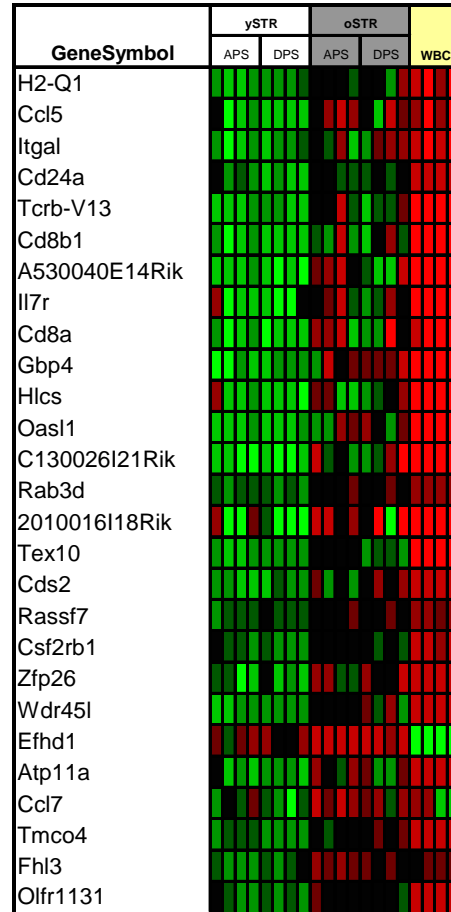


Figure 6. Heat maps for the most differentially regulated genes (FDR<10%) from microdissected prostate stroma. **A)** Intrinsic smooth-muscle/fibroblastic stroma transcriptional profile. Genes whose signal intensity in the white blood cells (WBC) was higher than 800 were removed and listed in figure B. Note the high expression of several genes in the old stroma (oSTR) compared to young stroma (ySTR) and white blood cells (WBC). **B)** Genes that were significantly up-regulated in the aged stroma that were also expressed in the white-blood cells with signal intensity levels higher than 800 (in WBC). Heat map colors reflect fold ratio values between sample and reference pool and mean-centered across samples. Columns represent biological replicates from dorsal and anterior microdissected cells for each age group and white-blood cells. Rows represent individual genes. Values shown in red are relatively larger than the overall mean; values shown in green are relatively smaller than the overall mean. Unpaired, two-sample t-test was used to identify significant genes. $P < 0.05$ was considered significant.

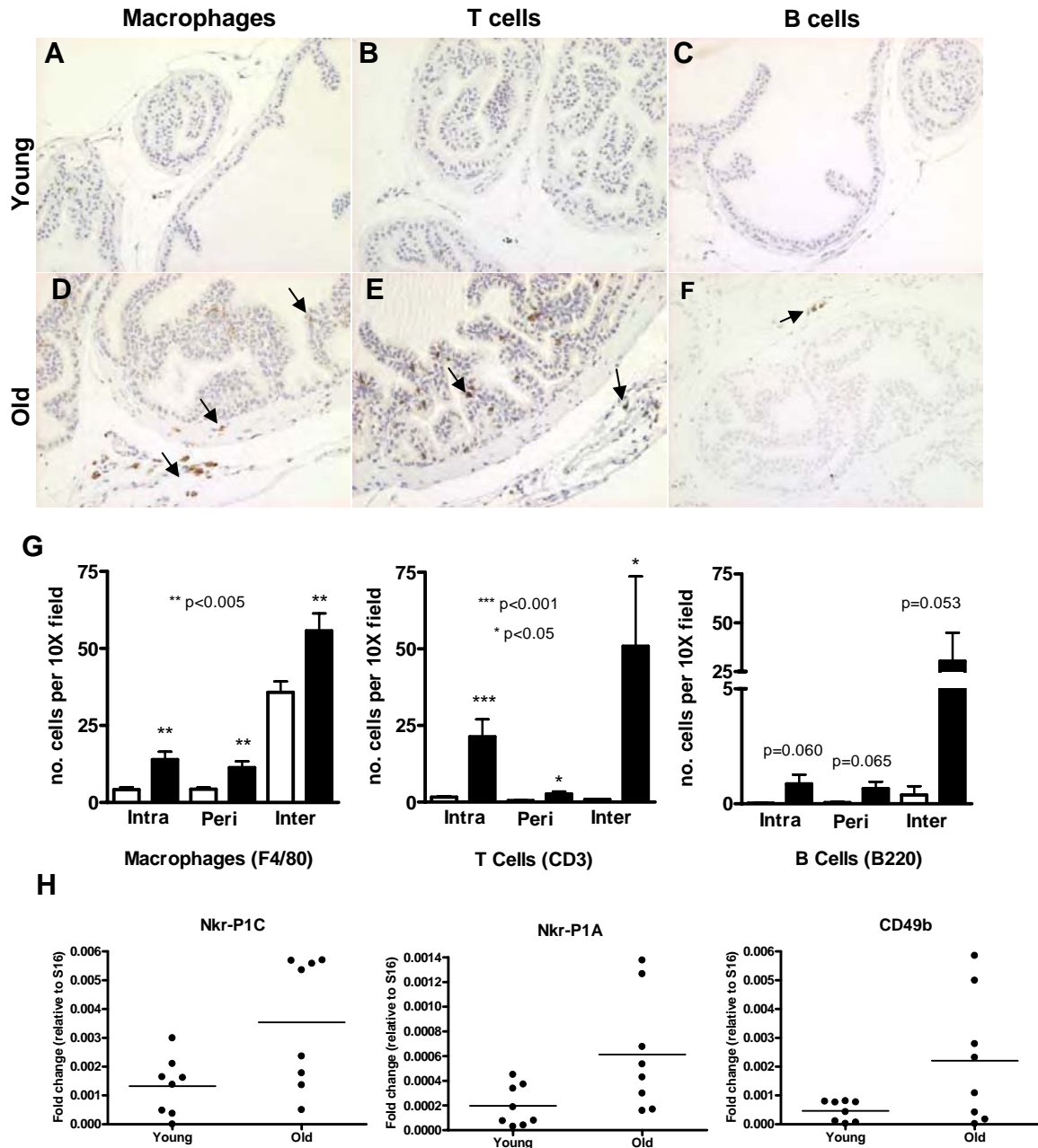
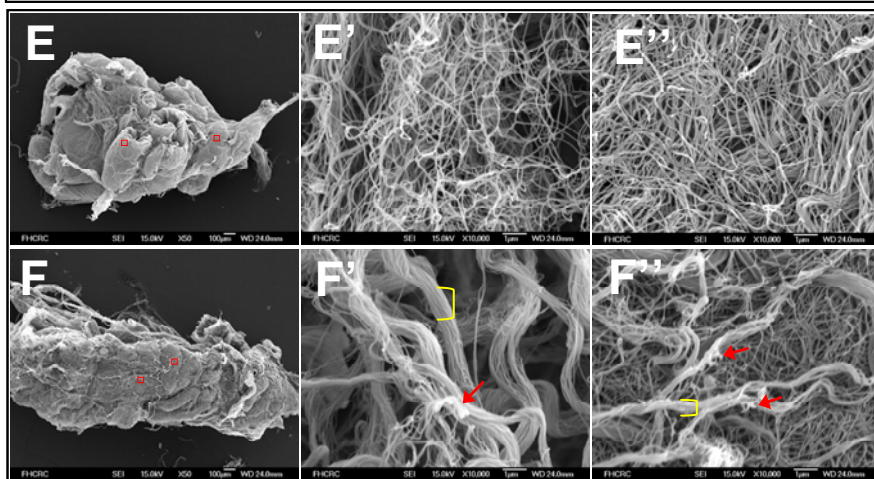
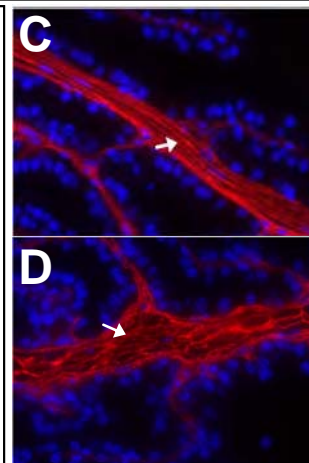
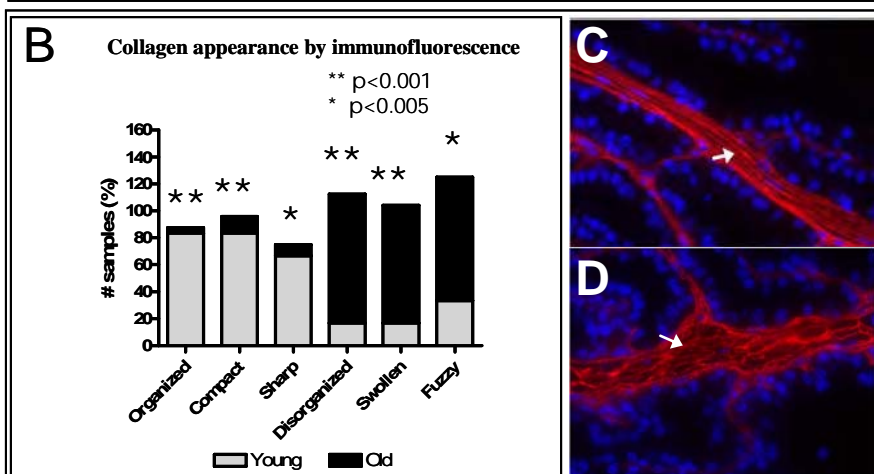
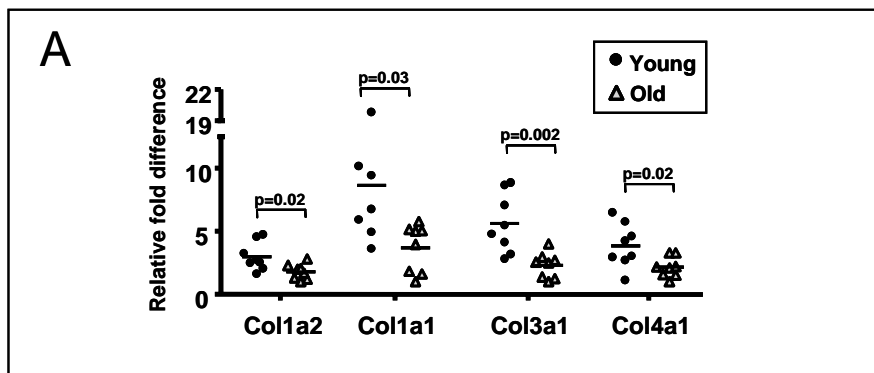


Figure 7. Prevalence of inflammatory cells in prostates from aged mice. A-F) Immunohistochemical analysis of 4μM paraffin sections from anterior prostate of young (A-C) and old (D-F) mice. Sections were stained with anti-F4/80 (A and D) anti-CD3 (B and E) and anti-B220 (C and F), which recognize macrophages, T cell and B cells, respectively. IHC demonstrated a high number of inflammatory cells within the aged prostate tissue. **G)** The number of cells positive for each immune-cell marker were determined by the number of cells/10X field on each lobe by blinded section analysis from young (4 month-old; n=10) and old (24 month-old; n=13) prostate sections. Inflammatory infiltrates were divided into three different categories: intraglandular infiltrates (inflammatory cells in contact with the glandular luminal epithelium); periglandular stromal infiltrates (inflammatory cells in contact with the smooth-muscle/fibroblastic cellular stroma); and interglandular infiltrates (inflammatory cells in the interglandular space). Data are mean ± standard error for all lobes combined. ***p<0.001; **p<0.005 and *p<0.05. **H)** Analysis of NK-cells specific markers: Nkr-P1C, Nkr-P1A and CD49b transcripts levels by qRT-PCR from micro-dissected young (n=8; 4-month-old) and old (n=8; 24-month-old) anterior and dorsal prostate stroma. Ribosomal S16 transcript expression levels were used to normalize qRT-PCR data. p<0.05 for all three genes tested.

Figure 8. Age-related collagen alterations. **A)** qRT-PCR for Col1a2, Col1a1, Col3a1 and Col4a1 from RNA isolated from microdissected stroma from young (n=8; 4-month-old) and old (n=8; 24-month-old) anterior prostate. The down-regulation of these procollagen genes verified the microarray analysis. Circle: young and triangle: old. Ribosomal S16 transcript expression levels were used to normalize qRT-PCR data. Normalized results are expressed relative to the lowest expressing value for each gene tested. **B-D)** Qualitative and quantitative confocal microscopy analysis for the appearance of collagen fibers in young and old mouse prostate. Thirty micrometers sections of anterior prostate lobes were stained by immunofluorescence with Collagen Type I and were evaluated by confocal microscopy in order to obtain a stack of images inside the intact tissue. Six scoring criteria were used to quantify the differences in collagen fiber appearance (organized, compact, sharp, disorganized, swollen and fuzzy collagen fibers). Five young and five old anterior prostates from independent mice were used and 4 images were taken from each sample. **C, D)** Representative images of Collagen Type I immunofluorescent stain of frozen sections from 4- (C) and 24-month (D) old mice (Magnification: 40x). Note the coarse and fragmented appearance and less regular distribution of collagen fibers in old prostates compared to the fine collagen fibers and highly organized network in the young prostate (arrows). **E-F)** Scanning Electron Microscopy of acellular preparations from young (E) and old (F) anterior prostate. E and F) General view of the anterior prostate from young (e) and old (f) mice. **E'-F'')** Representative images of high power fields from young (E' and E'') and old anterior prostate. Note the collagen meshwork of loosely woven fibrils with an intact structure of distinct collagen bundles in the young prostate (E' and E'') compared to the adhered collagen bundles (brackets) and fragmentation of collagen fibrils (arrows) in aged prostate (F' and F''). This phenotype was observed in all analyzed samples and in different selected random field (young n=5 and old n=5).



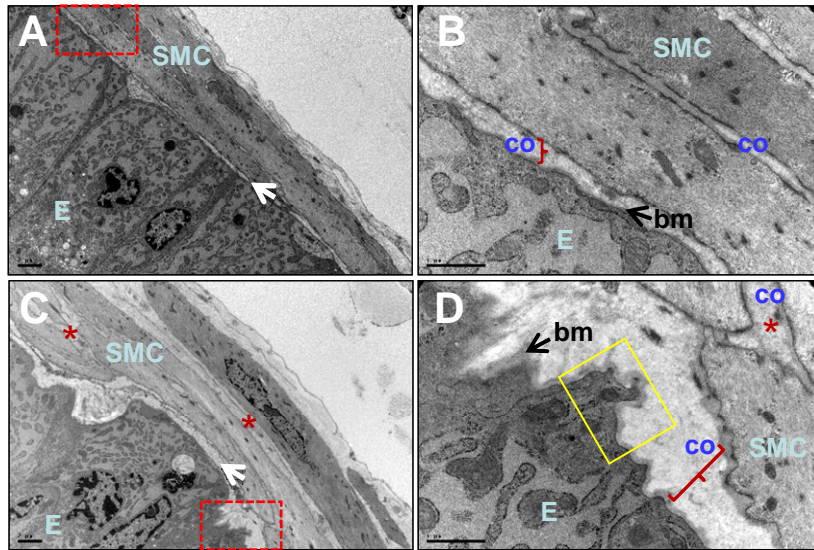


Figure 9 Ultrastructure of the young and old mouse prostate. Transmission electron microscopy of cross sections from young (A, B) and old (C, D) normal mouse prostate. **A and C)** general view of the glandular-adjacent stroma in proximity to the prostatic epithelium (E). Red dashed square: region presented in B and D. **B and C)** Detail of the epithelial-stromal interface in young (B) and old (D) prostates with a thick basement membrane (bm). A thick layer of collagen fibrils (co and brackets) are distributed at the epithelium base and interspersed with smooth muscle cells (SMC). The bm in aged prostate presents undulations (yellow square and arrow) provoked by the compression of cytoplasmic projections of epithelial cells. Yellow square: Detail of an epithelial cell (E) with cytoplasmic expansions compressing the basement membrane, implying a more favorable matrix for the invasion of epithelial cells towards the extracellular matrix. **E** indicates luminal epithelial; **SMC**, smooth muscle cells; **bm** and arrow, basement membrane; **co** and brackets: collagen fibrils. These sections are representative of sections obtained from 4 prostates for each age group.

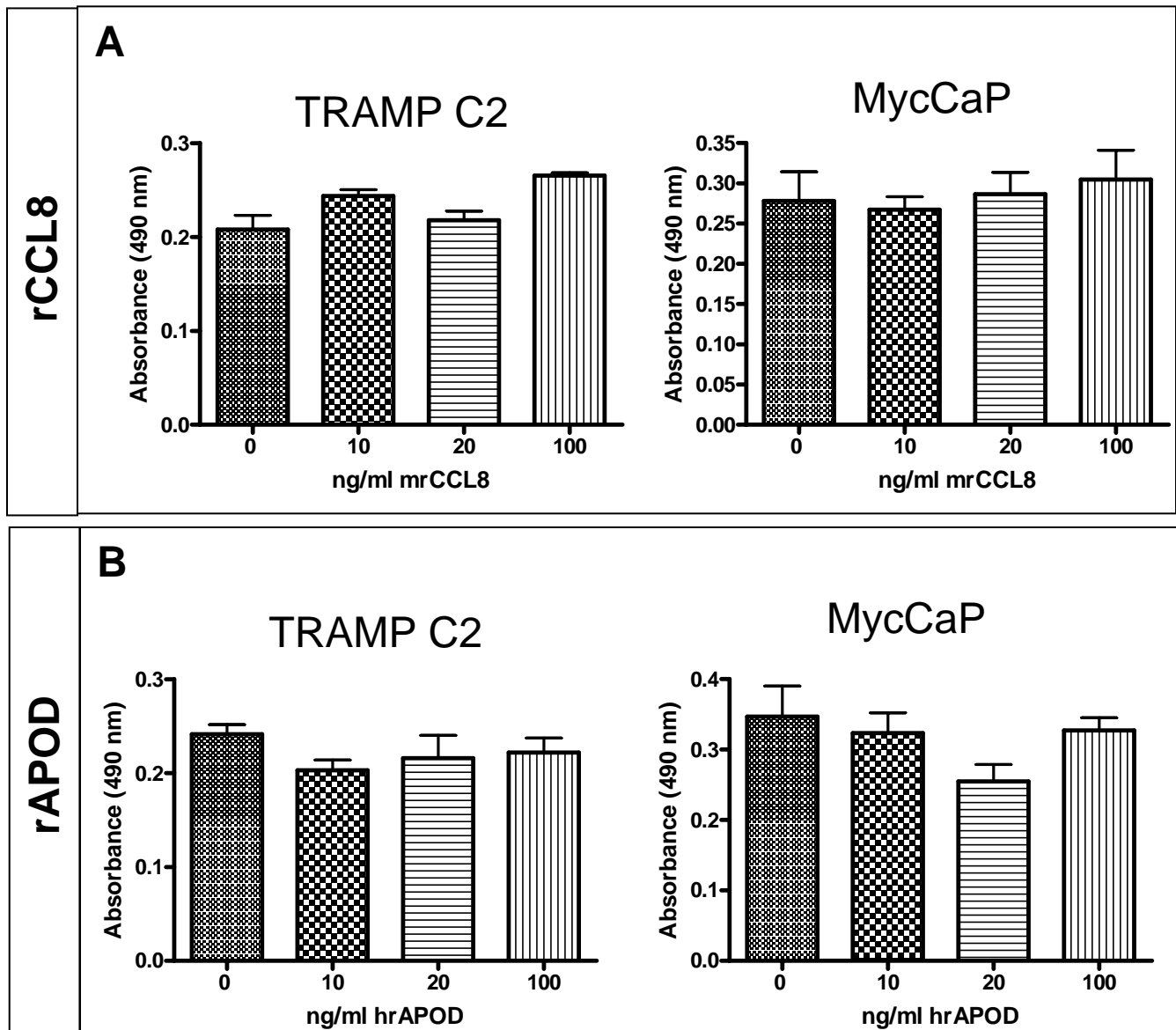


Figure 10. Recombinant CCL8 or APOD did not alter the growth of prostate tumor cells. Increasing concentrations of recombinant CCL8 (A) or APOD (B) were added to seeded mouse TRAMP C2 (TC2) and MycCaP (Myc) tumor cell lines in DMEM and 5% FBS media. The cultures were incubated for 24 hours and viable cell numbers were determined by the colorimetric MTS assay. All proliferation assays were performed in triplicate.

Figure 11. Representative images from the collaborative work performed with Dr. Reed⁴⁵, showing the differences in collagen fibril formation, fibril size, density and contraction between collagen extracted from young and old mice.

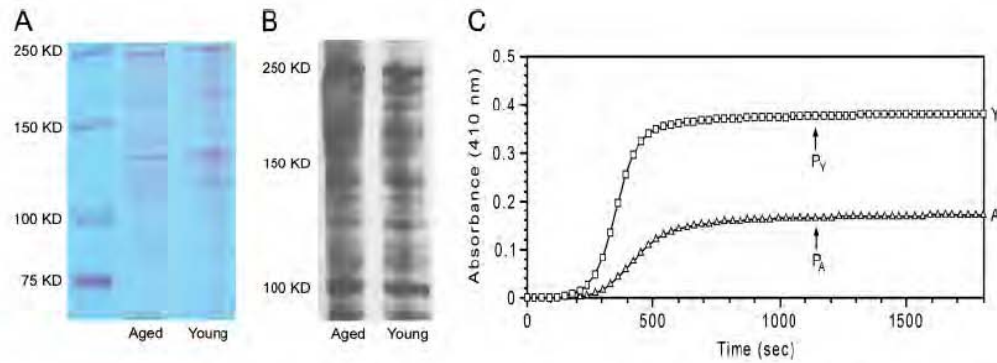


Figure 1. Gel profiles and polymerization of young and aged collagen extracts. Collagen extracts from young (Y) and aged (A) mice have similar band patterns, as visualized by Coomassie blue stain (panel A). Immunoblot using an antibody against collagen I (panel B) showed no significant differences in quality or quantity of the bands. Subsequent polymerization assay demonstrated that native collagen extracted from young mice (Y—squares) initiates fibril formation earlier and at a greater rate than corresponding collagen extracted from aged mice (A—triangles). The absorbance plateau (P_Y) of young mouse collagen is substantially higher than that of aged mouse collagen (P_A), indicating a more effective assembly of collagen molecules into fibrils (panel C).

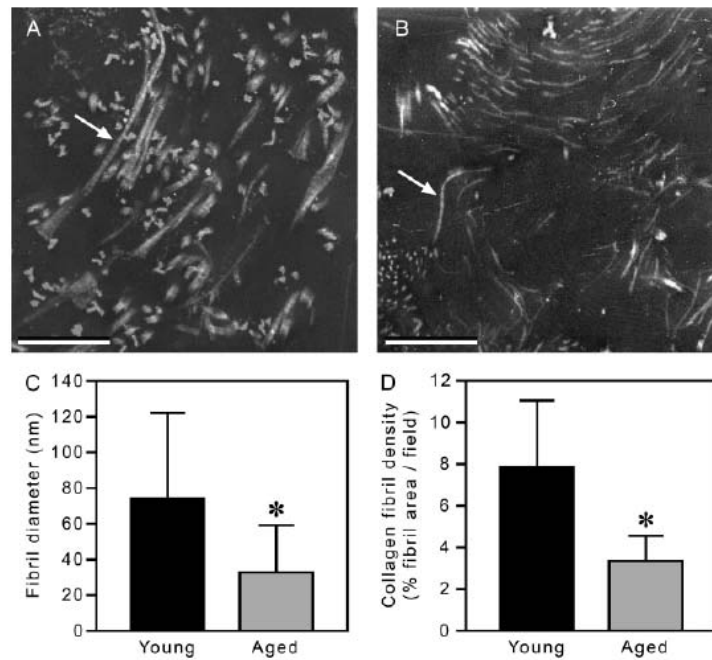


Figure 2. Transmission electron microscopy analysis of three-dimensional (3D) gels made from young and aged collagen. There are more young collagen fibrils (panel A, an example is indicated by an arrow) with greater diameters than aged collagen fibrils (panel B, arrow). Quantification of the images confirmed that 3D gels made from young collagen have thicker fibrils (75 vs 34 nm, respectively, panel C) at a higher density (8% vs 3.5% area, respectively, panel D) than corresponding gels made from aged collagen. In A and B, bars = 500 nm. In C and D, data are shown as mean \pm standard deviation; * $p < .02$.

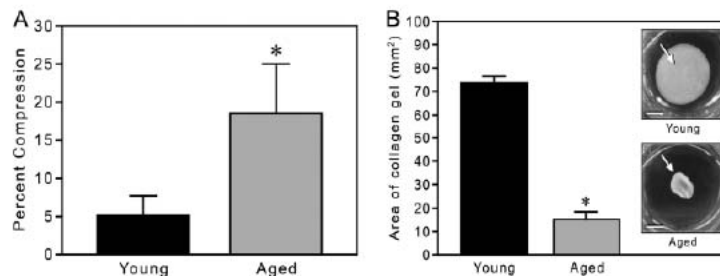


Figure 3. Malleability and gel contraction of three-dimensional gels made from young and aged collagen. Fully polymerized 0.6 mg/mL collagen gels were compressed by centrifugation for 10 minutes at 375g. Under elevated gravity, collagen from aged mice is more compressible than that from young mice (19% vs 5% compression, respectively). Data are shown as mean \pm standard deviation; * $p < .02$ (panel A). Collagen gels (0.6 mg/mL) from young and aged mice were then populated with human dermal fibroblasts and cultured for 18 hours (panel B). The cells contracted the aged collagen significantly more than the young collagen (15.5% vs 73% area, respectively). Bar graph data are shown as mean \pm standard deviation; * $p < .01$. Insets show young and aged collagen gels (arrows), respectively, after the contraction period (bars = 3 mm).

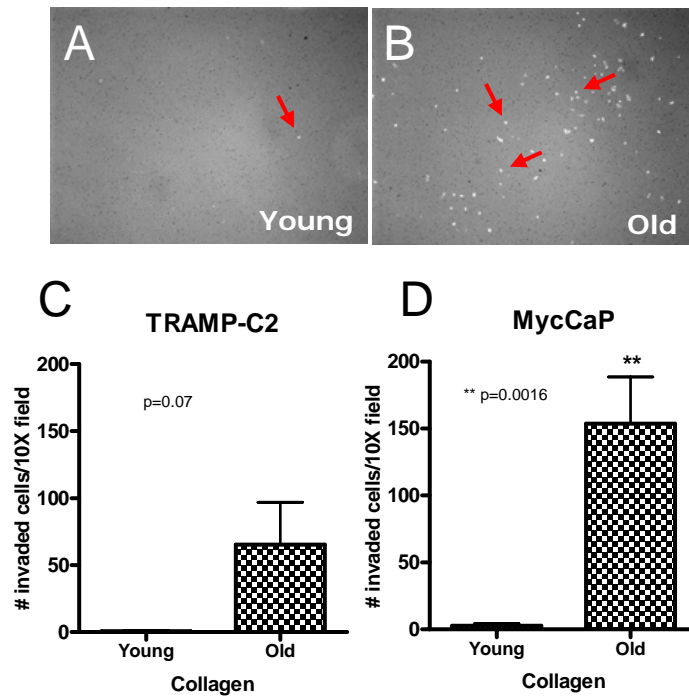


Figure 12. Enhanced invasion of prostatic malignant cells in old collagen. A and B) Lower surfaces of the invasion membrane showing Myc-CaP cells after invading 3D collagen gels harvested from tail tendons from young (A) and old (B) mice. Note the higher number of cells (arrows) that invaded through the old collagen compared to young collagen. **C and D)** Quantitated numbers of invaded TRAMP-C2 (C) and Myc-CaP (D) cells. The number of Myc-CaP cells that invaded through the old collagen (153.5 ± 35.12 cells/10x field, N=6) was significantly higher compared to young collagen (2.833 ± 1.493 cells/10x field, N=6) $p=0.0016$ (d). Similar results were observed with TRAMP-C2 cells however the difference was not significant (young collagen 0.8333 ± 0.4014 cells/10x field, N=6; Old collagen 65.33 ± 31.80 cells/10x field, N=6; $p=0.07$) (C). Data are mean \pm standard error.

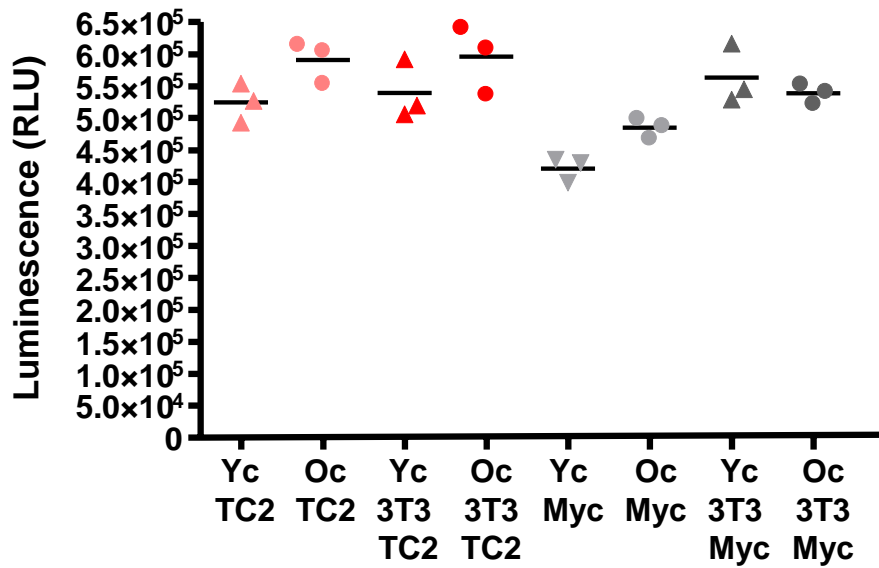


Figure 13. Proliferation of TRAMP-C2 and MycCaP mouse prostate cancer cell lines in young and old collagen matrices after 24 hours. Cells were plated within 3D collagen gels and allowed to attach and grow for 24 hours. After 24 hours proliferation was determined using the Cell Titer-GLO assay. **Yc**: collagen matrix extracted from young (4 month-old) mouse tail tendon. **Oc**: collagen matrix extracted from old (20-24 month-old) mouse tail tendon. **TC2**: TRAMP-C2 cells. **Myc**: MycCaP cells. **3T3**: mouse fibroblasts. Experiments were performed in triplicate.

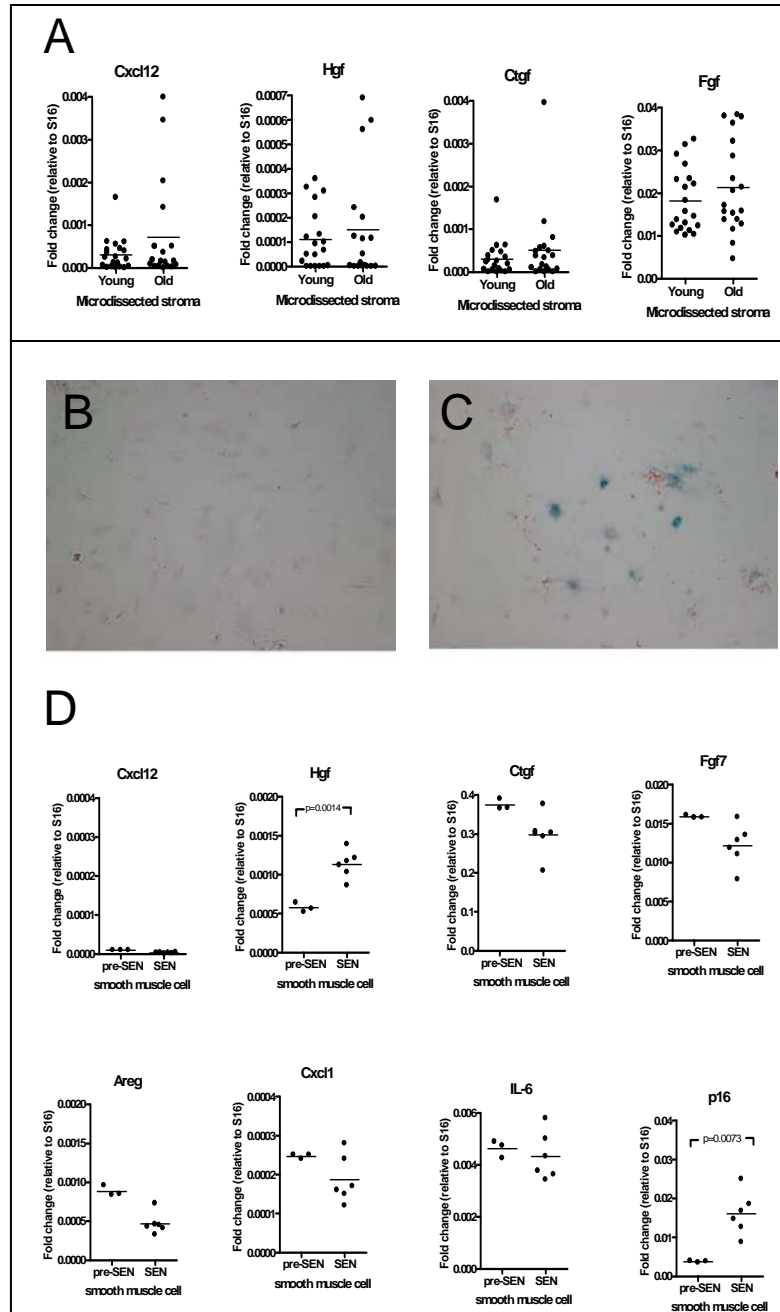


Figure 14. (A). qRT-PCR for selected senescence-associated factors. RNA is from microdissected stroma from young and old mice. B-C) pre-senescence (B) and senescent (C) prostatic smooth-muscle cells, demonstrating positive SA-B-Gal stain after H₂O₂ treatment. D. qRT-PCR for selected senescence associated secretory factors.

Table 1. Gene expression changes in the mouse prostate stroma from young (4 month-old) and old (24 month-old) C57BL/6 mice. White blood cells expression subtracted. Fold change values are averages of the anterior and dorsal prostate measurements from the Agilent microarray analysis. Positive values indicate an increase, and negative values indicate a decrease in gene expression in the old prostate. Gene names in bold appear to be novel and not previously reported to be altered with in vivo aging (n) or in vitro senescence.

Symbol	Gene name	Fold Change (Old/Young)	GO Function
Raly1	RALY RNA binding protein-like	+36	nucleic acid binding
Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	+9	serine-type endopeptidase inhibitor activity
Trp63	transformation related protein 63	+7.2	transcription factor activity
Slc26a3	solute carrier family 26, member 3	+6.9	anion exchanger activity; sulfate porter activity
BC020489	cDNA sequence BC020489	+6.5	
LOC432593	Hypothetical gene supported by AK078606	+6.1	
5330417C22Rik	RIKEN cDNA 5330417C22 gene	+6.1	
Ccl8	chemokine (C-C motif) ligand 8	+4.6	chemokine activity; heparin binding
Gylt1b	glycosyltransferase-like 1B	+3.9	transferase activity\, transferring hexosyl groups
Krt15	keratin 15	+3.8	structural constituent of cytoskeleton
Fmo3	flavin containing monooxygenase 3	+3.7	dimethylaniline monooxygenase (N-oxide-forming) activity;disulfide oxidoreductase activity
Pkp1	plakophilin 1	+3.1	cell adhesion molecule activity;intermediate filament binding;structural constituent of epidermis
Rnmt	RNA (guanine-7-) methyltransferase	+2.9	RNA binding;mRNA (guanine-N7-)-methyltransferase activity
KIAA0746	KIAA0746 protein	+2.6	
B930041F14Rik	RIKEN cDNA B930041F14 gene	+2.4	
Apod	apolipoprotein D	+2.3	high-density lipoprotein binding;lipid binding;lipid transporter activity
Olfir971	olfactory receptor 971	+2.3	
Grhl1	grainyhead-like 1 (Drosophila)	+2.2	
Tsku	leucine rich repeat containing 54	+2	
Inadl	InaD-like (Drosophila)	+2	ATP binding;protein binding;structural constituent of ribosome
Tcl1b2	T-cell leukemia/lymphoma 1B, 2	+2	
Car1	carbonic anhydrase 1	+1.9	carbonate dehydratase activity;zinc ion binding
Clcc1	chloride channel CLIC-like 1	+1.9	
Vgll3	RIKEN cDNA 1700110N18 gene	+1.9	
Rorc	RAR-related orphan receptor gamma	+1.8	steroid hormone receptor activity;transcription factor activity
Pak3	p21 (CDKN1A)-activated kinase 3	+1.7	ATP binding;protein serine/threonine kinase activity;protein-tyrosine kinase activity
Perp	PERP, TP53 apoptosis effector	+1.7	structural constituent of eye lens
Snx26	sorting nexin 26	+1.7	GTPase activator activity;protein transporter activity
Sectm1b	secreted and transmembrane 1	+1.6	
LOC628746	Similar to RING1 and YY1 binding protein	+1.6	
BC050196	cDNA sequence BC050196	+1.6	
Olfir788	olfactory receptor 788	+1.5	
Ccdc106	coiled-coil domain containing 106	-2.37	
Grik4	glutamate receptor, ionotropic, kainate 4	-2.71	glutamate-gated ion channel activity;kainate selective glutamate receptor activity;potassium channel activity

ABSTRACT

Poster title: “Expression Profiles of the Aged Prostate Microenvironment Identify Alterations in Transcripts Encoding Extracellular Matrix Proteins: Implications for Prostate Carcinogenesis” Presented at the Translational Research at the Aging and Cancer Interface (AACR) February 20-23, 2007.

Expression Profiles of the Aged Prostate Microenvironment Identify Alterations in Transcripts Encoding Extracellular Matrix Proteins: Implications for Prostate Carcinogenesis

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Background: The greatest single risk factor for the development of prostate adenocarcinoma is advanced age. Emerging evidence suggests that molecular alterations in the aged prostate microenvironment mediated by stromal aging and senescence are key factors regulating carcinogenesis and neoplastic progression. However, no functional studies have been reported that definitively provide mechanistic evidence of cause and effect. To investigate the role of the aged-stroma microenvironment in prostate carcinogenesis, we profiled the molecular changes in gene expression that occur with aging in the normal murine prostate stroma.

Methods: We performed gene expression profiling using RNA isolated from micro-dissected benign mouse prostate stroma from young (n=5; aged 4 months) and old (n=5; aged 24 months) animals. RNA was amplified and hybridized to a mouse prostate-specific cDNA microarray. Age-associated differential expression of candidate transcripts was confirmed by quantitative RT-PCR and immunohistochemistry.

Results: Expression profiling demonstrated clear differences in gene expression between old and young prostate stroma, with 39 genes exhibiting significant transcript abundance levels ($p < 0.005$). Transcripts encoding extracellular matrix components for Type I and Type III collagen (Col1a2, down 4-fold and Col3a1 down 3-fold, respectively) were among the genes most substantially altered with aging. Quantitative RT-PCR confirmed the lower expression of Col1a2 and Col3a1 in the aged prostate stroma. Interestingly, although immunofluorescence detection for Type-I and Type-III collagen did not show substantial differences at the protein level between young and old prostate tissue, it revealed a disorganized collagen matrix in the aged prostate microenvironment when compared to young prostate.

Conclusions: Gene expression differences are evident between young and aged prostate stroma. The disorganized collagen matrix and the diminished expression of Col1a2 and Col3a1 in the aged prostate microenvironment may have an effect on the structural and signaling properties of the extracellular matrix. In turn, a dysfunctional ECM in the aged prostate could plausibly facilitate carcinogenesis and neoplastic progression.

ABSTRACT

Talk title: “Studies of Normal Variation and the Aged Microenvironment in the Prostate: Implications for Prostate Cancer”. FHCRC. December 10th, 2009. Seattle, WA.

Prostate cancer is a health problem worldwide. Family history, race and age represent the greatest contributors for developing prostate cancer. In this dissertation, I examined histological and molecular phenotypes of the normal prostate, in the context of genetic background and aging, to identify features that could influence the development, progression and metastasis of prostate cancer.

Studies of prostate carcinogenesis in rodent models have demonstrated modifications of cancer rates dependent on the host genotype, suggesting that features of benign tissues, present prior to cancer initiation, could modify tumorigenesis. I used microarray analysis to quantitate transcript levels in the normal prostates of five inbred mouse strains and found that 932 genes ($FDR \leq 10\%$), including genes previously shown to influence cancer, exhibited differential expression across strains. Analyses of human prostate transcripts orthologous to variable murine prostate genes identified differences in gene expression in benign epithelium that correlated with the aggressiveness of adjacent tumors, suggesting that a predisposition exists prior to cancer initiation.

Despite the strong correlation between aging and prostate cancer, the mechanism(s) underlying this relationship remains unknown. In a comparison of young (4 month) and old (20-24 month) mice, I identified significant changes in the expression of 1259 genes ($p < 0.05$) in the prostatic stroma that associated with normal aging in vivo. These included over-expression of genes associated with inflammation, genotoxic/oxidative stress and soluble factors and, down-regulation of pro-collagen genes. I demonstrated that aged prostates exhibit a disrupted collagenous matrix and aged collagen induced the invasion of prostate cancer cells in vitro. Immunohistochemical studies revealed an enrichment of inflammatory cells in aged

prostates. Together, these findings demonstrated that during normal aging the prostate exhibits phenotypic and molecular characteristics that are also associated with malignancies. I found that prostate cancer cells injected intraprostatically into young and aged mice resulted in higher tumor weight and metastatic spread in the aged host, suggesting that the aged microenvironment presents a permissive context for the growth and metastatic spread of cancer cells. Together, this work provides new information regarding age-associated alterations of potential importance in prostate carcinogenesis, and advances a functional system in which therapeutic strategies can be evaluated.

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The Effects of Aging on the Molecular and Cellular Composition of the Prostate Microenvironment

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Keywords: aging, prostate cancer, mouse, extracellular matrix, inflammation, smooth muscle

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ABSTRACT

BACKGROUND: Advancing age is associated with substantial increases in the incidence rates of common diseases affecting the prostate gland including benign prostatic hyperplasia (BPH) and prostate carcinoma. The prostate is comprised of a functional secretory epithelium, a basal epithelium, and a supporting stroma comprised of structural elements, and a spectrum of cell types that includes smooth muscle cells, fibroblasts, and inflammatory cells. As reciprocal interactions between epithelium and stromal constituents are essential for normal organogenesis and serve to maintain normal functions, discordance within the stroma could permit or promote disease processes. In this study we sought to identify aging-associated alterations in the mouse prostate microenvironment that could influence pathology.

METHODOLOGY/PRINCIPAL FINDINGS: We quantitated transcript levels in micro-dissected glandular-adjacent stroma from young (age 4 months) and old (age 20-24 months) C57BL/6 mice, and identified a significant change in the expression of 1259 genes ($p < 0.05$). These included increases in transcripts encoding proteins associated with inflammation (e.g., *Ccl8*, *Ccl12*), genotoxic/oxidative stress (e.g., *Apod*, *Serpinb5*) and other paracrine-acting effects (e.g., *Cyr61*). The expression of several collagen genes (e.g., *Colla1* and *Col3a1*) exhibited age-associated declines. By histology, immunofluorescence, and electron microscopy we determined that the collagen matrix is abundant and disorganized, smooth muscle cell orientation is disordered, and inflammatory infiltrates are significantly increased, and are comprised of macrophages, T cells and, to a lesser extent, B cells.

CONCLUSION/SIGNIFICANCE: These findings demonstrate that during normal aging the prostate stroma exhibits phenotypic and molecular characteristics plausibly contributing to the striking age associated pathologies affecting the prostate.

INTRODUCTION

Mammalian aging is associated with molecular, cellular and physiological changes characterized by a deteriorating homeostatic balance associated with the increasing prevalence of neoplasia and other diseases. At the molecular level, aging has been associated with an increase in DNA point mutations, telomere attrition, and alterations in patterns of methylation [1,2,3], each of which can disrupt the normal expression and/or function of proteins involved in cellular growth, maintenance of genomic integrity, responses to cellular stress, and inflammation [4,5]. Replicative senescence (RS)—associated with telomere erosion, and stress-induced premature-senescence (SIPS)—induced by oxidative stress, oncogene activation or DNA damage, have also been linked to the aging process (Reviewed in [6,7]). Paradoxically, while strong evidence supports cellular senescence as a protective mechanism that inhibits unrestrained cell proliferation and carcinogenesis in the young, it may favor the development of neoplasia and other pathology in the elderly [8]: several studies have demonstrated that concomitant with the loss of ability to replicate, senescent cells secrete an assortment of growth factors, inflammatory cytokines and extracellular matrix proteins that together create a local tissue microenvironment capable of inducing inflammation and promoting the growth of initiated or preneoplastic cells [9,10,11].

In man, many of the most common diseases involving the genitourinary tract are strongly associated with advanced age. These include benign hyperplasia of the prostate gland (BPH)---30% of men over age 50, the spectrum of Lower Urinary Tract Symptoms (LUTS), and prostate adenocarcinoma. Autopsy studies indicate that prostate cancer incidence approaches 60-70% in the 8th and 9th decade of life [12,13]. A relationship between aging and inflammation, hyperplasia and neoplasia of prostatic tissue has also been observed in rodents and dogs [14,15,16,17]. Overall, the etiology of these diseases remains poorly defined despite causing substantial morbidity and mortality in the population.

The prostate gland is composed of secretory luminal epithelium, basal epithelium, neuroendocrine cells and cell types comprising a supporting stroma. The stroma in the human and rodent prostate gland consists primarily of smooth muscle cells and fibroblasts with rarer populations of endothelium, nerve cells, and infiltrating inflammatory

cells [18,19]. The tissue microenvironment plays important roles in producing a spectrum of autocrine/paracrine factors as well as structural molecules that maintain normal cell behavior and organ homeostasis [20,21,22]. Accumulating evidence points towards a role for aging-related changes in constituents comprising the prostatic stroma in promoting prostate epithelial cell growth, though most of this evidence is derived from *ex vivo* experimental systems. *In vitro* studies of fibroblasts isolated from prostates of older men were less able to suppress epithelial cell proliferation than fibroblasts isolated from the prostates of younger men [23]. When co-cultured with premalignant prostatic epithelial cells, senescent prostatic fibroblasts promote epithelial cell growth, and this proliferative response is in part due to the overexpression of secreted paracrine-acting factors [11]. These findings suggest that alterations in the prostate microenvironment, mediated by events associated with stromal aging and/or senescence, permit and/or promote epithelial responses that contribute to organ pathologies.

The objective of this study was to systematically define and quantitate histological and molecular features of the prostatic microenvironment that associate with normal aging *in vivo*. We hypothesized that molecular alterations determined through studies of *in vitro* senescence would be evident in the context of advanced organismal age, supporting a role for this cellular program in prostatic diseases. An inbred mouse strain was selected in order to control for genetic and environmental variables that could confound the interpretation of aging phenotypes. We used expression microarrays to quantitate transcript abundance levels in the stromal compartment of the prostate and evaluated immune cell subtypes and structural features by immunohistochemistry and electron microscopy, respectively.

RESULTS

Effects of age on prostate cellular composition and morphology

To evaluate the cellular composition of the prostate gland in the context of normal aging, we resected the prostate glands from mice of the C57BL/6 strain aged 4-months, designated young, and 24-months, designated old. We used 4 month-old mice as our young cohort because at this age the males are sexually mature, and therefore less prone to ex-

hibit subsequent changes associated with organogenesis and developmental processes. After dissection the prostates were fixed, embedded in paraffin, sectioned, and stained with hematoxylin and eosin (H&E) for histological studies. Each prostate lobe was individually compared across age groups. Overall, each lobe showed subtle differences in morphology with aging (representative images are shown in **Figure 1**). In contrast to young mice, focal atrophy of a small number of acini as well as epithelial atypia coexisted with morphologically normal acini in old mice. The cellular stroma layer adjacent to the epithelial cells (glandular-adjacent stroma) was generally more disorganized in old animals than in young animals with little evidence of consistent smooth muscle cell directional orientation and evidence of rounding of smooth-muscle and fibroblast cells within the extracellular matrix (**Figure 1**., brackets and inset). Foci of inflammatory infiltrates comprised of cells with characteristic small cell size and little cytoplasm were observed in the interductal stroma and appeared more abundant in the prostates from old animals (**Figure 1**, arrows).

To determine the cell composition of the glandular-adjacent stroma we stained prostate sections from young and old mice by double immunofluorescent staining for smooth-muscle-actin and vimentin (a mesenchymal cell type marker). We determined that 95% of the adjacent stromal cells stained positive for smooth-muscle actin and only 5% stained positive for vimentin (see **Supporting information Figure S1**). Thus, the majority of the glandular-adjacent cellular stroma in the mouse prostate is represented by smooth muscle cells, consistent with prior studies of murine and human prostates [18,19,24]. No significant difference in the ratio of cell types expressing these markers was found between young and old prostates. Of note, there was no overlap between smooth muscle actin-positive and vimentin-positive cells, consistent with the lack of a myofibroblast cell type in normal prostate tissue, in both young and old animals.

Effects of age on gene expression in prostatic stroma

A key objective of this study centered on the analysis of aging-related molecular changes in cell types comprising the stromal compartment of the prostate. To evaluate the ability of laser-capture microdissection (LCM) to acquire pure cell populations, we performed a pilot study using LCM to separately isolate luminal epithelial cells and glan-

dular-adjacent stroma from young (n=5) and old mice (n=5). We opted to capture cells from the anterior and dorsal lobes since, based on histology, these two lobes have the most abundant cellular smooth-muscle/fibroblastic stroma (**Figure 1**, brackets). In addition, the anterior and dorsolateral lobes have also been reported to be the regions in which prostate intraepithelial neoplasia (PIN) and prostate carcinogenesis begins in murine models [25,26,27,28,29] and gene expression data indicates that the dorsolateral lobe is most homologous to the peripheral zone of the human prostate, where cancer is most prevalent [30]. We verified cell-type specific purity by analyzing the expression levels of known stromal cell and epithelial cell markers using a customized mouse prostate cDNA array (MPEDB array) [31]. Three biological replicate pools per lobe, representing five 4 month-old and five 24 month-old animals, were generated to facilitate statistical analyses and control for individual variability. As expected, stromal and epithelial transcripts were differentially expressed in the stroma and epithelial samples respectively (**Figure 2A,B**). To further characterize the relationships between the epithelial and stroma samples and between age groups, we performed Principal Component Analysis (PCA) for all the genes in the arrays (**Figure 2A**). PCA clearly grouped a subset of genes that discriminated the epithelial and stroma samples, suggesting that the major differences between samples resulted from the differential expression of large numbers of genes between the stroma and epithelial compartments. These results demonstrate that highly enriched populations of stroma cells can be isolated by microdissection.

We next compared transcript abundance levels in the epithelial and stromal cell compartments and identified 378 and 282 genes to be differentially expressed with aging in the stroma and epithelial samples respectively, as determined by a Student's T-test analysis ($p < 0.05$) (**Figure 2C and 2D**). To verify the aging-induced gene expression alterations in prostate stroma, we performed an additional microarray experiment from laser captured microdissected adjacent stroma from an independent set of 4 month-old (n=12) and 24 month-old (n=12) C57BL/6 mice and used a more comprehensive microarray platform comprised of oligonucleotides complementary to ~40,000 genes. Using the same t-test cutoff ($p < 0.05$), 718 transcripts were increased and 541 transcripts decreased in aged versus young prostate stroma (**Supporting information Figure S2**). A significant correlation coefficient of 0.22 ($p < 0.0001$) between the two distinct microarray

experiments was determined using the scored T-test for the most differentially expressed genes in both platforms ($p < 0.05$). Experiments using qRT-PCR as an independent measurement confirmed that chemokine (C-C motif) ligand 8 (*Ccl8*) and apolipoprotein D (*Apod*) were increased in aged prostate stroma (**Figure 3A and 3B**, respectively). We also determined that *Apod* and *Ccl8* are expressed at very low levels in white blood cell isolates and in microdissected epithelium relative to stroma, and no differences were seen between young and old epithelium. Several genes were identified with lower expression in aged relative to young prostate stroma including transcripts encoding extracellular matrix proteins *Colla1*, *Colla2*, *Col3a1*, among others. We confirmed lower expression levels of these collagen genes by qRT-PCR (see below).

Since histological analysis demonstrated that the aged prostate contains a higher number of inflammatory cells, we were concerned that a component of the aged prostate stroma expression profile could reflect transcripts derived from infiltrating leukocytes. We generated expression profiles from purified white blood cells from C57BL/6 mice (WBC) and compared the expression levels of each age-associated stromal gene with abundance levels in the WBC preparation (**Figure 4**). Considering the most significant up- and down-regulated genes ($p < 0.05$) in the aging data set we found that 59% of the genes determined to be altered in aging stroma overlap with genes expressed in the white blood cell profile. These results suggest that a large component of the age-associated gene expression changes may reflect infiltrating cells (**Figure 4B**), but that substantial changes are also intrinsic to the aging process of the smooth-muscle/fibroblastic stroma and not from differences in numbers of infiltrating leukocytes (**Figure 4A and Table 1 and Table 2**). To further evaluate this concept, we examined the prostate glands of young and aged mice of the ICR/SCID strain housed in a barrier facility. In the absence of infiltrating lymphocytes and neutrophils in the prostates of these mice, we confirmed that age-associated changes in smooth muscle cell histology and aging-associated gene expression occurred (e.g. 2-fold increase in *Apod* expression; $p < 0.05$) (**Supporting Information Figure S3**). However, these animals were not formally isolated in a pathogen-free environment, and more rigorous attention to sterility and the elimination of other immune-cell components will be required to evaluate the complex interactions between environment and intrinsic aging.

Correlations between *in vivo* aging and *in vitro* senescence

Although the molecular process of replicative senescence is intimately associated with features of aging, it has been challenging to directly determine whether senescent cellular phenotypes normally accumulate with aging in numbers sufficient to influence pathological processes *in vivo*. We selected several genes known to be associated with *in vitro* senescence and compared their transcript levels between young and aged prostate stroma. The first cohort we evaluated were those comprising a senescence-associated secretory phenotype (SASP) shown to directly influence epithelial cell growth [11]. Unexpectedly, none of the senescence associated candidate factors we evaluated, *Hgf*, *Ctgf*, *Fgf7*, *Cxcl12*, *Areg*, *Il6*, *Il1a*, and *Cxcl1* were up-regulated in the aged mouse prostate stroma (see **Supporting information Figure S4**, for genes whose transcripts were detectable in microdissected stroma). However, transcripts we found to be elevated in aged stroma *in vivo*, such as *Apod* and *Ccl8*, were also up-regulated in primary human prostate fibroblasts that were induced to senesce *in vitro* (**Figure 3C**).

Employing a more systematic approach, we compared the transcriptional profiles of aged murine stroma measured in this study (considering a false discovery rate of <25% and including those transcripts also found in leukocytes), with previously determined transcriptional profiles of human prostate fibroblasts induced to senesce by different means (H_2O_2 , Bleomycin, replicative senescence, overexpression of p16 and overexpression of oncogenic RAS [11] and unpublished data). Of 264 genes significantly altered in aged mouse stroma, 37 genes were also significantly altered in at least one senescence profile (FDR<25%) (**Supporting information Figure S5**). Genes involved in the NF- κ B pathway, such as *STAT1* and *TLR1*; cell proliferation/apoptosis, such as *IER3*; *EHF*; *LRPAP1* and inflammation such as *CCL7*; *CXCL16*; *B2M*; *IL7R* and *LGALS3* were among the genes whose transcripts were increased in the context of both *in vivo* aging and *in vitro* senescence. The changes within these gene groups are in agreement with the age-enriched biological functions identified by pathway-based analyses described below.

Prostate aging influences specific molecular pathways

To determine if the age-induced gene expression alterations comprised specific biological programs, we used gene set enrichment analysis (GSEA) to determine the statistical asso-

ciations of predetermined gene cohorts. We used the Gene Ontology (GO) set (C5) and curated gene sets (C2) which included canonical pathways, and a senescence-associated gene list generated based on gene expression changes quantitated in human prostate fibroblasts [11]. We found 164 GO gene sets to be significantly enriched in the aged stroma (FDR<25%). These included enrichment of ‘Inflammatory Response’ and ‘Cytokine/Chemokine Activity’ categories (NOM P-value <0.05; FDR <2%). Genes involved in the ‘NF-κB Cascade’ were also enriched in the aged stroma (NOM P-value <0.05; FDR <25%), consistent with prior studies linking intracellular regulation of immune responses in both aging and age-related diseases [32]. GSEA also determined that the category of ‘collagen binding and collagen genes’ was significantly enriched for transcripts downregulated in aged stroma (NOM p-value<0.05 FDR <25%). Additionally, using the database of curated gene sets, we found that gene sets derived from aged mouse neocortex, cerebellum, kidney and retina were enriched as well as the senescence-associated gene list derived from senescent prostate fibroblasts (NOM p-value <0.05 FDR <25%). GenMAPP 2.1 was used to visualize the age-associated expression changes in pathways found significant by GSEA. A representation of the Cytokine and Inflammatory response pathway is shown in **Supporting Information Figure S6**.

Effects of aging on prostate extracellular matrix components and tissue architecture

The transcript profiling studies determined that genes encoding structural extracellular matrix components were expressed at lower levels in aged relative to young prostate stroma. These included several collagen-encoding genes; collagen I $\alpha 1$ and $\alpha 2$ subunits, and collagen III $\alpha 1$ subunit. We confirmed significantly lower transcript levels of *Colla1*, *Colla2*, *Col3a1* and *Col4a1* in aged stroma by qRT-PCR (**Figure 5A**). To further investigate these findings, we used fluorescence and ultrastructural microscopic analysis to determine the relationship between collagen structure and aging. Examination of the extracellular matrix (ECM) surrounding prostate epithelial cells by immunofluorescent staining for Type I collagen and picrosirius red (a selective staining agent for collagen; data not shown) demonstrated that the majority of the stroma around the prostatic ductal structure is fibrillar collagen (**Figure 5B and 5C**). Interestingly, although immunofluorescence detection for Type-I collagen did not show substantial differences in

the protein abundance between young and old prostate tissue, it revealed a disorganized collagen matrix network with a coarse, fragmented, and less ordered distribution of the collagen fibrils in prostates from old animals compared to the fine collagen fibrils and highly organized network in prostates from young animals (**Figure 5C** and **5B**, respectively). In order to rule out that the disorganization of the collagen fibers was due to mechanical damaging during sectioning, 30µm sections of the anterior prostate lobe were stained by immunofluorescence with antibodies recognizing Type I collagen and were evaluated by confocal microscopy in order to obtain a stack of images inside the intact tissue. Six scoring criteria (see materials and methods section) were used to quantify the differences in collagen fiber appearance (organized, compact, sharp, disorganized, swollen and fuzzy collagen fibers). Collagen fibril appearance was significantly different between young and old prostates, with more than 70% of the aged prostates evaluated having disorganized, swollen and fuzzy collagen fibers ($p<0.05$) compared to the organized, compact and sharp collagen fibril appearance from young mice ($p<0.005$) (**Figure 5D**). Similar alterations were observed in sections from the dorsal, lateral and ventral lobes; however, to quantify the observations, the more abundant stroma layer in the anterior lobe was chosen to facilitate the scoring.

To investigate in greater detail the structural alterations of the collagen network in the aged prostate, we performed scanning electron microscopy using prostates from young and old animals. To visualize the three-dimensional organization of the collagenous stroma, samples were treated with serial washes of 10% NaOH solution to remove all cellular elements [33,34]. The acellular preparations (**Figures 6A** and **6B**) showed that a smooth and grossly homogeneous fibrous network lines the empty acinar space. Due to difficulties imaging the internal ducts of the acini it was not possible to assess whether this surface exhibits differences between young and old prostates. However, on the outside of the ducts, a sponge-like organization was apparent. The young prostates displayed a meshwork of loosely woven fibrils comprised of distinct collagen bundles, while in aged mice collagen bundles were adherent or joined to each other (**Figures 6Ai-Aii** and **6Bi-Bii**, respectively). These observations were similar to those seen by immunofluorescence staining for Collagen Type I (**Figure 5B** and **5C**). Collectively,

the collagenous stroma in the aged mouse prostate is characterized by a disorganized and disrupted collagen matrix.

To further characterize the prostate at the ultrastructural level, we performed transmission electron microscopy (TEM) analysis of young and old mouse prostates (**Figure 6C** and **6D**, respectively). In agreement with the immunofluorescence analysis for Collagen Type I, we found that despite the lower levels of procollagen I alpha-1 mRNA in the aged animals, they also exhibited a dramatic increase in collagen fibers in the stroma as determined by TEM (compared **Figure 6Ci** and **6Di**, brace). Additionally, since we demonstrated that the basement-membrane-codifying pro-collagen Col4a1 mRNA was down-regulated with aging (**Figure 5A**), we then analyzed the organization of the basement membrane by TEM in young and aged prostates. Although we did not find any obvious structural alterations or disruptions in the basement membrane between age groups, we did observe epithelial cytoplasmic projections extending towards the extracellular matrix in the aged prostate (**Figure 6Di**, yellow square), suggesting that the aged basement membrane is less rigid, thus allowing these epithelial cells to compress it towards the extracellular matrix. Consistent with these findings, similar ultra-structural phenotypes have recently been observed in the aged Mongolian gerbil ventral prostate [35]. In addition to the collagen changes, we also sought to determine whether the cells (mainly smooth muscle cells) within the altered extracellular matrix presented proper organization. In aged prostates, the smooth muscle cells presented a less consistent orientation within the stroma and did not have a continuous parallel arrangement as observed in young prostate (**Figure 6D-Di**, asterisk, and **6C-Ci**, respectively).

Effects of normal aging on prostate inflammation

The gene expression changes measured in the stroma of aged mouse prostate was indicative of a pro-inflammatory environment. Increased expression of inflammation-associated genes suggested that the stroma cells in the older animals were both responding to, and producing inflammatory signals. We next evaluated prostate tissues from aged (n=10) and young (n=10) animals for several markers that specify inflammatory cell types: F4/80 (macrophages), CD3 (T cells) and B220 (B cells) (**Figure 7A-F**), and determined that the number of B cells, T cells and macrophages were significantly in-

creased in the aged prostate (B cells, $p=0.049$; T cells, $p=0.003$; Macrophages $p<0.001$; **Figure 7G**). We then evaluated the localization of these immune cells and determined the number of cells positive for each immune cell marker. Inflammatory infiltrates were divided into three different categories: periglandular stromal infiltrates (inflammatory cells in contact with the smooth-muscle/fibroblastic cellular stroma); intraglandular infiltrates (inflammatory cells in contact with the glandular luminal epithelium); and interglandular infiltrates (inflammatory cells between glands). The number of intraglandular, periglandular, and interglandular macrophages and T cells were significantly higher in aged prostates compared to young prostates ($p<0.05$) (**Figure 7G** and **Supporting information Figure S7**). There were low numbers of B cells in contact with the epithelium and smooth-muscle cells (range from 1-16 cells per 10x field) and B cells were absent in most prostatic regions in both young and aged mice. However, in the interglandular space, B cells were present in a significantly higher number in the aged prostate compared to young prostates ($p=0.053$) (**Figure 7G**). Although we did not stain the prostate gland for NK cells, higher levels of transcripts encoding NK specific markers (Nkr-PC1, Nkr-P1A and Cd49b) were found in the prostate tissue of the aged mice ($p<0.05$; data not shown). These observations, along with the increased expression of immune-specific genes (especially chemokines and immunoglobulin genes) are consistent with the increased infiltration of lymphocytes and macrophages in the aged mouse prostate.

The elevated numbers of inflammatory cells in the aged prostate prompted us to investigate the potential reasons for this finding. By H&E staining of prostate tissues from each age group, we were able to discard the possibility of an inflammatory response due to bacterial infections, since neither obvious bacteria nor associated neutrophilic infiltrates were present in the mouse prostates. Thus, one reason for the presence of the inflammatory cells in the aged prostate might be a consequence of increased levels of chemokines/cytokines originating from the aged smooth-muscle fibroblastic stroma. However, we cannot rule out the possibility that the transcripts encoding these cytokines, at least *Ccl7* and *Ccl5*, are derived directly from the infiltrating inflammatory cells in the stromal samples (**Figure 4B**). To date we have not been able to demonstrate whether the increased levels of chemokines, such as *Ccl8* in aged prostate originate exclusively from smooth-muscle/fibroblastic cellular compartment or includes a contribution from infiltrat-

ing cells. However, the fact that *Ccl8* and *Apod* were not expressed in the peripheral leukocyte populations isolated from young and old C57BL/6 mice, suggests that these alterations are likely to be intrinsic to the smooth muscle cells and fibroblasts.

DISCUSSION

Studies in humans and other mammals have shown that frequently encountered disorders of prostate growth, classified as benign prostatic hyperplasia (BPH) and prostate carcinoma, are associated with aging [36,37,38,39,40,41,42]. However, there is no established molecular explanation for the profound age-dependent increase in these diseases. Thus, our intent was to obtain an unbiased view of the histological and molecular changes in the microenvironment of the prostate gland that accompany advancing age, with a view toward defining those features capable of influencing prostatic pathology. To this end, we used an inbred mouse strain to isolate intrinsic aging-associated features from effects attributable to genetic variation, diet, or external environment.

Histological analyses of the prostate did not show quantifiable differences in the glandular compartment between young and old mice; however changes in the non-epithelial microenvironment were clearly evident with increased numbers of inflammatory infiltrates and a collapsed appearance of the smooth muscle cells present within the glandular-adjacent stroma. This observation is in agreement with studies in aged human skin where reduced fibroblast spreading has been proposed to be indicative of diminished mechanical tension due to a lack of direct association of the fibroblasts with age-related fragmented collagen fibrils [43,44]. These alterations in mechanical tension and cell shape have been suggested to be critical determinants of cellular function [45,46], implying changes in gene expression. Thus, we anticipated that smooth-muscle cells and fibroblasts in the aged prostate might exhibit alterations at the molecular level, reflecting age-related structural modifications, a response to the infiltration of inflammatory cells, or stemming from other intrinsic aging-related alterations.

In order to identify specific and consistent aging-associated alterations in gene expression in the glandular adjacent stroma, a region primarily comprised of smooth muscle cells, we used laser capture microdissection and full-genome transcript profiling to quan-

titate transcript abundance levels. In a comparative analysis between the microdissected stroma and epithelial cells we were able to show that little overlap exists in age-related gene expression between these two compartments, suggesting that aging phenotypes are not uniform in nature. Consistent with this concept, several studies have shown that patterns of gene expression associated with aging or senescence is strongly influenced by tissue type and/or cell lineage [47,48,49]. Analyses of gene networks encompassing the alterations observed between young and aged prostate stroma demonstrated a significant enrichment for inflammation pathways, the NF- κ B program, and collagens, among others. Consistent with these results, analyses of the aged rat prostate [37,38] as well as global studies using different tissues and species including mice and humans [50], identified greater expression of inflammatory and stress-response genes, along with a decrease in extracellular matrix components with age [50,51,52]. However, these studies could not determine which cellular compartment contributed to the expression changes, as they were performed using whole tissues. In contrast, our study demonstrated that genes up-regulated in the aged prostate, such as *Apod* and *Ccl8* were specifically associated with the stroma compartment and not the aged epithelium.

Using Gene Set Enrichment Analysis we determined that genes altered in human prostatic senescent fibroblasts are enriched in aged stroma, especially those involved in inflammatory responses. However, we also found that many of the key factors comprising the senescence-associated secretory program (SASP) [11] were not altered in the aged mouse stroma. This observation suggests that senescent cells do not accumulate in sufficient numbers with advancing age to contribute substantially to the expression profile of the composite transcriptome ascertained from the stroma. Alternatively, the smooth muscle cell phenotype that dominates the prostate stroma may engage an aging/senescence program distinct from that of fibroblasts.

Considering that inflammatory processes can induce cell stress and that stressed mesenchymal cells can secrete inflammatory chemoattractants [11,53], it remains to be determined whether inflammatory infiltrates are a cause of, or response to, the molecular alterations exhibited by aged stroma. While the chemokines *Ccl8*, *Ccl12*, *Ccl5* and *Ccl7* found to be elevated in the context of aging may directly promote inflammation, the specific influence of each of these cytokines in the prostate remains to be established. We

were able to demonstrate an increase in T cells, macrophages and to a lesser extent B cells in the aged prostate. These cells were not only present in clustered foci in the interglandular regions but were also found infiltrating into the smooth-muscle/fibroblastic stroma as well as the luminal epithelium, and could be effectors of age-related pathologies. A link between genotoxic stress and the activation of the innate immune system through NF- κ B has been proposed as a cause of premature aging [32]. Chronic inflammation has emerged as a potential risk factor for carcinomas in many organs such as the liver, colon, bladder, lung and pancreas [54], and there is compelling evidence supporting a role for inflammation in the pathogenesis of prostate cancer [55,56,57]. Thus, our observation demonstrating the prostate of aged animals harbors increasing numbers of immune cells suggests that aging correlates with a pro-inflammatory state which in turn may well influence prostate neoplasia.

A striking age-associated finding involved the development of an abundant, highly disorganized and fragmented collagen matrix in the prostate. These collagen alterations may be a consequence of age-associated changes of collagen cross-linking [58,59,60] and impairment of its degradation [61] rendering an accumulation of partially degraded fibrils [44]. Of relevance to the gene expression measurements, collagen fragmentation has been shown to promote oxidative stress [44] and could explain the increased expression of stress response genes, such as *Apod* as well as the increase in inflammatory infiltrates. Pertinent to the regulation of collagen in the prostate, androgen deprivation induces marked morphological changes in rat prostatic smooth muscle cells [62,63] reduces collagen synthesis, and induces a collagen fibrillar reorganization in the rat ventral prostate [64,65,66]. On the other hand, 17 beta-estradiol increases the accumulation of collagen in the prostate [67]. It is possible that the hormonal imbalance related to the aging process, together with the potential loss in mechanical tension of the smooth-muscle cells in the aged prostate stroma, as observed by classic histology and transmission electron microscopy, may well affect collagen synthesis and organization.

While the descriptive characteristics of the collagen network are important in our understanding of structural changes with aging, their functional role(s) and biological relevance in prostate pathology remain to be elucidated. In this context, recent evidence supports collagen content, cross-linking, fiber structure, and organization, as key determi-

nants of tumor cell behavior: higher collagen density was shown to increase tumorigenesis, local invasion, and metastasis of mammary epithelial cells, causally linking an increase in stromal collagen to tumor formation and progression [68]. In the human prostate, the collagen tissue network appears to be altered in prostate pathologies (BPH and adenocarcinomas) [34], resembling in part the morphological changes in the collagen matrix observed in the normally aging mouse prostate. These changes at the ultrastructural level may have implications for prostate growth in normal and pathologic states, though mechanistic cause-effect studies will be required to confirm this hypothesis. In this context, collagen type IV has been shown to enhance the growth of rat ventral prostatic epithelial cells *in vitro* [69], and type I collagen mediates proliferative responses of prostate carcinoma cells [70].

In summary, the studies of the murine prostate microenvironment reported herein demonstrate consistent molecular and structural changes that accompany advancing age. Future studies should be directed toward confirming that these alterations also associate with advancing age in the human prostate gland, and determining which alterations are influenced by genetic variation and which can be modified by environment. Though distinct from the robust senescence program observed *in vitro*, the dysregulated cytokines, stress-response factors, and matrix components identified *in vivo* may causally influence prostate pathologies and should be considered for intervention strategies that could delay or reverse the onset of BPH, LUTS, and prostate cancer.

MATERIALS AND METHODS

Ethics Statement

All animal studies were approved by the Institutional Animal Care and Use Committee at the Fred Hutchinson Cancer Research Center, IR#1671.

Tissue acquisition and microdissection

Young (4 month-old) and old (20-24 month-old) C57BL/6 male mice were obtained from the National Institutes of Aging (NIA) Rodent Colony at Harlan Sprague Dawley (Chicago, IL) and cared for in accordance with approved IACUC protocols. For studies

of immunocompromised mice, two month-old ICR-SCID male mice were obtained from Taconic and maintained and aged in a barrier facility. Mice in the barrier suite were housed in sterilized microisolator cages using Allentown HEPA-filtered and ventilated racks. Work done in these rooms took place within a HEPA-filtered hood. Animals were sacrificed and prostate tissue dissected when they reached the desired age: 4 months and 13 months for young and old mice respectively. Following shipment, mice were acclimated to a common temperature, day-night cycle, and diet for at least 12 days to minimize environmental differences. Mice from each age group were randomized for the day and time of sacrifice. Following halothane anesthesia, mice were sacrificed by cervical dislocation. Prostates were rapidly excised, immersed in OCT embedding compound (Miles Diagnostics, Elkhart, Ind., USA) and snap-frozen in liquid nitrogen and stored at -80° C.

Frozen sections (7 μ M) from young and aged animals were cut from OCT embedded snap-frozen mouse prostate glands into PAP-membrane slides and immediately fixed in 95% ethanol for five minutes, washed in deionized RNase-free water, and stained with Mayer's hematoxylin for 30 seconds, followed by another water wash. The sections were then dehydrated with two five-minute washes in 100% EtOH. Approximately 10,000 glandular-adjacent stroma cells were separately captured from the anterior and dorsal prostate lobes from 17 independent animals of each age group as well as anterior and dorsal prostate luminal epithelium from 5 animals in each age group using the Veritas LCM system (Arcturus Mountain View, CA). Digital photos were taken of tissue sections before, during, and after LCM and assessed independently to confirm the cell type-specificity of the captured cells. To control for individual mouse variability [71], the microdissected stromal samples were combined for total RNA isolation into four pools representing three mice from each aged group and prostatic lobe. Prior to microarray hybridization, cell-type specific purity was verified by qRT-PCR using primers for known stromal (smooth muscle-actin, vimentin) and epithelial (probasin) markers.

Gene expression analysis by microarray hybridization

All data is MIAME compliant, and the raw data have been deposited in a MIAME compliant database, the Gene Expression Omnibus (GEO) database, as detailed on MGED

Society website <http://www.mged.org/Workgroups/MIAME/miame.html>, and is available at www.ncbi.nlm.nih.gov/geo, under accession GSE21542.

Total RNA from LCM experimental samples were isolated using the Arcturus PicoPure RNA Isolation kit (Molecular Devices, Sunnyvale, CA) incorporating DNase-treatment using the RNase-Free DNase Set (Qiagen Inc, Valencia, CA.). To provide a reference standard RNA for use on two-color cDNA microarrays, we pooled total RNA isolated from normal adult male Swiss-Webster mice (10% prostate and 30% each testis, liver, and kidney.) Reference RNA was purified using Trizol (Life Technologies, Rockville, MD) following the manufacturer's protocol followed by further purification by RNeasy maxi kit (Qiagen Inc, Valencia, CA) including DNase treatment using the RNase-Free DNase Set (Qiagen Inc, Valencia, CA.) Total RNA from experimental samples were amplified two rounds and reference total RNA was amplified one round using the Ambion MessageAmp aRNA Kit (Ambion Inc, Austin, TX), according to the manufacturer's specifications. The amplified RNA was used as template for cDNA probe synthesis followed by hybridization to a custom mouse prostate cDNA array (MPEDB array) composed of approximately 8,300 genes expressed in the developing and adult mouse prostate [72], or to a 44K oligonucleotide microarray (Agilent, Inc). Probe synthesis, microarray hybridization and data acquisition were performed as described previously [31,73]. Spots of poor quality or average intensity levels <300 were removed from further analysis.

To identify genes that varied between young and aged mouse prostate, log₂ ratio measurements were statistically analyzed by a Student's T-test analysis (unpaired, two-tailed, unequal variance), and transcripts with p-values <0.05 were considered significantly altered between young and old stroma. Transcriptional profiles of the epithelium and stroma samples from young and old mice were also compared with Principal Components Analysis (PCA) using Bioconductor software [74].

To identify specific biological pathways that exhibit age specific alterations, microarray results were subjected to Gene Set Enrichment Analysis (GSEA) [75]. Genes were preranked based on the T-test score between young and aged mouse prostate. For genes represented by multiple probes, we used the T-test statistic from the probe that had the largest absolute T-test statistic. GSEA was run in preranked mode using the Gene Ontol-

ogy (GO) set (C5) and curated gene sets (C2) from the Molecular Signatures Database using 1000 permutations to estimate the false discovery rate to assess statistical significance. An FDR of < 25% was considered significant. GenMAPP 2.1 (www.genmapp.org) was used to visualize the age-associated expression changes in pathways found significant by GSEA. Gene expression changes of aged vs. young stroma is represented in either red (up in aged) or green (down in aged). More intense color is used to show genes significantly changed with p-value <0.05. Grey color indicates no change while white indicates gene not present.

White Blood cell collection and RNA extraction

Whole white blood cells samples were collected from young (4 month-old; n=5) and old (24 month-old; n=4) C57BL/6 mice by cardiac puncture under halothane anesthesia before sacrifice by cervical dislocation. Blood samples were kept on ice until fractionation. Blood was fractionated by centrifugation at 1400 rpm for 10 minutes at room temperature. Serum was removed, and the exposed white blood cells layer (or buffy coat) was carefully aspirated. The white blood cell preparations for each age group were pooled and treated with 10 ml of Hemolytic Buffer (NH_4Cl , 8.3mg/ml; NaHCO_3 1 mg/ml; Na_2EDTA 0.4 mg/ml) preheated at 37°C and incubated at room temperature for 10 minutes. Cells were pellet at 750 rpm and washed twice with PBS. Samples were store frozen at -80°C until RNA isolation. Total RNA extraction was performed using Qiagen RNeasy kit, following the manufacturer's protocol. Total RNA was amplified one round and the amino-allyl UTP incorporated using the Ambion MessageAmp aRNA Kit (Ambion Inc, Austin, TX), according to the manufacturer's specifications. The amplified RNA was used as template for cDNA probe synthesis followed by hybridization to a 44K oligonucleotide microarray (Agilent, Inc). The Mouse Gold Standard was used as a reference RNA in order to compare the white blood cell and the aging transcriptional profiles.

Quantitative RT-PCR

RNA from microdissected mouse prostate stroma and epithelium, and human prostate fibroblast (PSC27) were used as template for qRT-PCR. 200ng of amplified RNAs or 20 µg of total RNAs, respectively, were used to generate cDNAs. SYBR GREEN real-time

PCR was performed as previously described [71]. Primers to ribosomal protein S16 (for mouse samples) and RPL13 (for human samples) were used to normalize cDNA loading. The sequences of the primers used in this study are in Table S1 (supporting information).

Immunohistochemistry

Formalin-fixed, paraffin-embedded mouse prostate tissue sections were deparaffinized, and endogenous peroxidase activity was blocked with 3% H₂O₂ for 8 min. Antigen was retrieved by steam heating with 10 mM citrate buffer (pH 6.0) for 20 min. Primary antibodies and working dilutions were as follows: Rat anti-CD3 (1:500, Serotech MCA1477); Rat anti-B220 (1:1000, Chemicon CBL1342); Rat anti-F4/80 (1:50, Serotech MCA497GA). After incubation of the primary antibody for 1 hour, slides were washed and incubated for 30 minutes with biotinylated species-specific secondary antibody (Biotin-SP conjugated Goat Anti-Rat IgG (H+L); 1:200, Jackson ImmunoResearch 112-065-167), washed, and then incubated with avidin-peroxidase complex (ABC, Vector Laboratories) for 30 minutes and visualized using DAKO Dab system. The sections were dehydrated, and permanently mounted. Species-specific IgG isotype were added in lieu of primary antibody as controls, and these sections demonstrated no detectable staining. Immunoreactive cells with CD3, F4/80 and B220 antibodies were counted under 10X fields. The number of each cell is recorded separately with regards to its location (intraglandular vs. periglandular vs. interglandular) within each lobe.

Immunofluorescence and Confocal Microscopy

OCT-embedded frozen prostates from five young (4 month-old) and five aged (24 month-old) mice were used for staining. Briefly, 7 µm and 30 µm sections, for light and confocal microscopy respectively, were fixed with 4% formaldehyde for 8 or 20 minutes, respectively. After fixation, the tissue sections were permeabilized with 0.1% Triton X-100 in Dulbecco's phosphate-buffered saline (PBS) for 10 minutes, followed by 3 washes with PBS. Tissue sections were exposed to a blocking solution consisting of 1X Super-Block Reagent and 5 % Normal Goat Serum in PBS for 1 hour. Next, the sections were

treated with primary antibody in blocking solution overnight at 4°C. Primary antibodies and working dilutions were as follows: Type I collagen (1:100, Rockland Inc. 600-401-103), vimentin (1:700, Abcam. ab45939). After three subsequent washing steps (5 minutes each), the primary antibody was visualized with goat anti-rabbit IgG secondary antibody bound to Alexa Fluor 488 (Invitrogen, Carlsbad, CA) in blocking solution and incubated for 1 hour. For vimentin-smooth muscle staining, sections were simultaneously stained for smooth-muscle actin using anti-Smooth Muscle-Cy3 (1:200, Sigma C6198) along with the secondary antibody. After four additional washing steps (5 minutes each), cover slips were mounted onto the microscope slides with anti-fade mountshield containing DAPI. Sections of 7 μ M were examined by light-fluorescence microscopy. Sections of 30 μ M were stained with Collagen Type I and visualized by confocal microscopy. In brief, stacks of confocal images were acquired on a Zeiss LSM 510 NLO confocal and two-photon microscope (Carl Zeiss, Inc. Thornwood, NY) fitted with a Zeiss 40x/1.3 PlanNeofluar oil immersion objective. The following laser lines and emission filters were used: DAPI: two photon excitation at 780 nm, 435-485 nm bandpass detection; 594 AlexaFluor: 543 nm excitation, 565-615 nm bandpass emission. Maximum intensity projections of selected confocal sections were obtained with Zeiss LSM software or ImageJ. Collagen fiber appearance of prostatic stroma of anterior lobe in five young and old mice was compared using 4 images from each sample taken at 400X magnification. Qualitative criteria assessing the structure of collagen were devised as follows. The collagen fibers were classified as organized when the fibers had continuous, evenly spaced, mostly parallel pattern and disorganized when the architecture appeared haphazard. The individual fibers were defined as compact when the fibers were delicate, their thickness was even and swollen when the relative thickness increased and fibers became coarse. In addition, each fiber was identified as sharp when the edges of the fibers were smooth or fuzzy when irregularities were observed. Images were independently scored by three individuals (including one pathologist) and a consensus was obtained.

Electron Microscopy

For transmission EM, fragments of prostate lobes were fixed by immersion with 1/2 strength Karnovsky's fixative (2% Paraformaldehyde/ 2.5% Glutaraldehyde in 0.2M Cacodylate buffer). After washing with 0.1 M Cacodylate buffer, fixed tissues were treated with 2% osmium tetroxide buffered in 0.2 M cacodylate buffer for 3 hours. Specimens were washed again and dehydrated in graded ethanol series (35% to 100% ethanol) and 2x propylene oxide and embedded in Epon resin. Ultrathin sections were cut and contrasted with uranyl acetate for 2 hrs, followed by lead citrate for 5 min. The samples were observed and evaluated with a JEOL 1230 transmission electron microscope. For scanning EM, whole prostate lobes (n=5 young and n=5 old) were fixed by immersion with 1/2 strength Karnovsky's fixative (2% Paraformaldehyde/2.5% Glutaraldehyde in 0.2M Cacodylate Buffer). Fixed tissues were immersed in 10% sodium hydroxide for 6 days to remove cellular constituents (the solution was changed daily). The acellular preparations were then washed for several hours in distilled water. After rinsing, the samples were fixed in 1% tannic acid overnight, rinsed again in distilled water and post-fixed in 1% Osmium tetroxide for 3 hours. Specimens were then dehydrated in graded concentrations of ethanol, critical-point-dried, mount onto stubs and sputter coated with Au/Pd. The samples were evaluated and imaged with a JEOL JSM-5800 scanning electron microscope with an acceleration voltage of 15kV, WD of 24.0 mm and tilt separation of 7-8°.

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FIGURE LEGENDS

Figure 1. Histological features of prostate glands from young and old mice.

Hematoxylin and eosin-stained sections of formalin-fixed prostate tissues from young (4 month-old) and old (24 month-old) mice. E: Luminal epithelium; S: Stroma adjacent to the epithelial cells (glandular-adjacent stroma). Note the thick glandular-adjacent cellular stroma (S, bracket) observed in dorsal and anterior lobe from young and old mice. AP insert: smooth-muscle cells (circled in white) appear less elongated and more rounded in the aged prostate with little evidence of cell orientation. Areas of inflammatory cell infiltration were observed frequently in the prostates of old animals (arrows). AP: anterior prostate; DP: dorsal prostate; LP: lateral prostate and VP: ventral prostate. (Magnification: 20x)

Figure 2. Age and cell type-specific transcript profiles in the mouse prostate.

A) Principal Component Analysis (PCA) for microdissected dorsal prostate stroma and epithelium from young and old animals. PCA discriminates epithelial and stromal samples. **EO**: old epithelium; **EY**: young epithelium; **SO**: old stroma; **SY**: young stroma.

B) Transcript abundance levels (Log2 Ratios) obtained from microarray-based measurements for genes known to exhibit preferential expression in stromal or epithelial cells. Red indicates increased expression; green indicates decreased expression. **C)** Heat map of age-associated transcripts in the prostate stroma ($p < 0.05$) compared to epithelium. Insert: Gene symbols for the 10 most up- and down-regulated genes in the aged stroma. **D)** Heat map of age-associated transcripts in the prostate epithelium ($p < 0.05$) compared to stroma. Insert: Gene symbols for the 10 most up- and down-regulated genes in the aged epithelium. Note the low correlation between the age-related profile of the stroma compared to the epithelium. Heat map colors reflect fold ratio values between sample and reference pool and mean-centered across samples. Columns represent biological replicates from microdissected dorsal and anterior epithelium and stroma for each age group. Rows represent individual genes. Values shown in red are relatively higher than the overall mean; values shown in green are relatively lower than the overall mean; rows shown

in brown are genes with no expression values. **STR**: microdissected glandular-adjacent stroma; **EPI**: microdissected luminal epithelium.

Figure 3. Expression of *Ccl8* and *Apod* with aging, senescence and cell type.

(A,B) Confirmation of stromal age-related changes in gene expression by qRT-PCR. RNAs were reverse transcribed and amplified using qRT-PCR with primers specific for *Ccl8* and *Apod*. RNAs analyzed: microdissected glandular-adjacent stroma (STR) and epithelium (EPI) from dorsal (n=4) and anterior (n=4) prostate lobes from C57BL/6 young (n=12) and old (n=12) mice used in microarray analyses. White blood cells (WBC) were isolated from young and old C57BL/6 mice (n=6). Note the higher expression of *Ccl8* and *Apod* in the microdissected old stroma (Old STR) compared to young stroma (young STR). Also notice the low abundance in transcript levels of these two genes in microdissected young and old epithelium (Young EPI, Old EPI, respectively) and in white-blood cells (WBC). **(C)** Human pre-senescent and senescent prostate PSC27 fibroblasts. Pre-SEN: pre-senescent cells; SEN (ASH) cells induced to senesce by H₂O₂ exposure; SEN (Bleo) cells induced to senesce by bleomycin exposure; SEN (Rad) cells induced to senesce by radiation exposure; RPL13 transcript expression levels were used to normalize the human qRT-PCR data.

Figure 4. Age and inflammatory cell associated gene expression changes in the mouse prostate stroma.

A) Intrinsic smooth-muscle/fibroblastic stroma transcriptional profile. Genes whose signal intensity in the white blood cells (WBC) was higher than 800 intensity units were removed and listed in panel B. Note the high expression of genes in the old stroma (oSTR) compared to young stroma (ySTR) and white blood cells (WBC). **B)** Genes significantly up-regulated in the aged stroma that were also expressed in white-blood cells with signal intensity levels higher than 800 intensity units (in WBC). Heat map colors reflect fold ratio values between sample and reference pool and mean-centered across samples. Columns represent biological replicates from dorsal and anterior microdissected cells for each age group and white-blood cells. Rows represent individual genes. Values shown in red are relatively larger than the overall mean; values shown in green are relatively

smaller than the overall mean. Gene lists represent the most significant up-regulated transcripts in old stroma compared to young stroma by unpaired, two-sample t-test analysis ($p < 0.05$) with fold changes higher than 2.2. APS=anterior prostate stroma; DPS=dorsal prostate stroma; WBC=white blood cells.

Figure 5. Age-related alterations in collagen expression and structure.

A) Analysis of Col1a2, Col1a1, Col3a1 and Col4a1 transcripts by qRT-PCR from micro-dissected young (n=8; 4-month-old) and old (n=8; 24-month-old) anterior prostate stroma. Circle: young; Triangle: old. Ribosomal S16 transcript expression levels were used to normalize qRT-PCR data. Normalized results are expressed relative to the lowest expression value for each gene tested. **B-D)** Qualitative and quantitative confocal microscopy analysis for the appearance of collagen fibers in young and old mouse prostate. Thirty micrometer sections of anterior prostate lobes were stained by immunofluorescence with Collagen Type I antibody and were evaluated by confocal microscopy. Six scoring criteria were used to quantify the differences in collagen fiber appearance (organized, compact, sharp, disorganized, swollen and fuzzy collagen fibers). Five young and five old anterior prostates from independent mice were used and 4 images were taken from each sample $**p < 0.001$ and $*p < 0.005$. **B, C)** Representative images of Collagen Type I immunofluorescent stain of frozen sections from 4- (B) and 24-month (C) old mice (Magnification: 40x). Note the coarse and fragmented appearance and less regular distribution of collagen fibers in old prostates compared to the fine collagen fibers and highly organized network in the young prostate (arrows).

Figure 6. Ultrastructure of the young and aged mouse prostate.

A and B) Scanning electron microscopy of acellular preparations from young (A) and old (B) anterior prostate. General view of the anterior prostate from young (A) and old (B) mice. **Ai-Bii)** Representative images of high power fields from young (Ai and Aii) and old (Bi and Bii) anterior prostate. Note the collagen meshwork of loosely woven fibrils with an intact structure of distinct collagen bundles in the young prostate (Ai and Aii) compared to the adhered collagen bundles (brackets) and fragmentation of collagen fi-

brils (arrows) in aged prostate (Bi and Bii). This phenotype was observed in all analyzed samples and in different selected random field (young n=5 and old n=5). **C and D)**

Transmission electron microscopy of cross sections from young (C, Ci) and old (D, Di) normal mouse prostate. C and D) general view of the glandular-adjacent stroma in proximity to the prostatic epithelium (E). Red dashed square: region presented in Ci and Di. Ci and Di) Detail of the epithelial-stromal interface in young (Ci) and old (Di) prostates with a thick basement membrane (bm). A thick layer of collagen fibrils ("co" and brackets) are distributed at the epithelium base and interspersed with smooth muscle cells (SMC). Yellow square: detail of an epithelial cell (E) with cytoplasmic expansions compressing the basement membrane. **E** indicates luminal epithelial; **SMC**, smooth muscle cells; **bm** and arrow, basement membrane; **co**: and brackets: collagen fibrils. These sections are representative of sections obtained from 4 prostates for each age group.

Figure 7. Prevalence of inflammatory cells in prostates from aged mice.

A-F) Immunohistochemical analysis of 4μM paraffin sections from anterior prostate of young (A-C) and old (D-F) mice. Sections were stained with anti-F4/80 (A and D) anti-CD3 (B and E) and anti-B220 (C and F), which recognize macrophages, T cell and B cells, respectively. IHC demonstrated a high number of inflammatory cells within the aged prostate tissue. **G)** The number of cells positive for each immune-cell marker were determine by the number of cells/10X field on each lobe by blinded section analysis from young (4 month-old; n=10) and old (24 month-old; n=13) prostate sections. Inflammatory infiltrates were divided into three different categories: intraglandular infiltrates (inflammatory cells in contact with the glandular luminal epithelium); periglandular stromal infiltrates (inflammatory cells in contact with the smooth-muscle/fibroblastic cellular stroma); and interglandular infiltrates (inflammatory cells in the interglandular space). Data are mean ± standard error for all lobes combined. ***p<0.001; **p<0.005 and *p<0.05.

Table 1. Genes with higher expression in the mouse prostate stroma from old (24 months) compared to young (4 months) C57BL/6 mice.

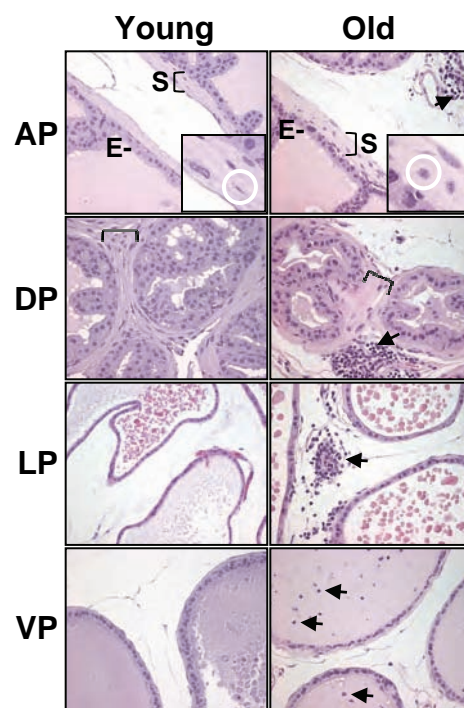
<i>Gene symbol</i>	<i>Gene name (abbreviated)</i>	<i>GenBank accession</i>	<i>Fold change (old/young)</i>
Raly1	RALY RNA binding protein-like	NM_178631	+ 35.9
Serpinb5	serine peptidase inhibitor, clade B, member 5	NM_009257	+ 9.0
Trp63	transformation related protein 63	NM_011641	+ 7.2
Slc26a3	solute carrier family 26, member 3	BC037066	+ 6.9
Apol9a	Apolipoprotein L 9a	AK050122	+ 6.5
Gm11538	predicted gene 11538	AK078606	+ 6.1
5330417C22Rik	RIKEN cDNA 5330417C22 gene	BC051424	+ 6.1
Fcgbp	Fc fragment of IgG binding protein	NM_176924	+ 5.9
Ccl8	chemokine (C-C motif) ligand 8	NM_021443	+ 4.6
Trim9	tripartite motif protein 9	AK163123	+ 4.6
Col17a1	procollagen, type XVII, alpha 1	NM_007732	+ 4.4
Coch	coagulation factor C homolog	NM_007728	+ 4.2
Ccl12	chemokine (C-C motif) ligand 12	NM_011331	+ 4.1
Gylt1b	glycosyltransferase-like 1B	NM_172670	+ 3.9
Nefh	neurofilament, heavy polypeptide	NM_010904	+ 3.9
Krt15	keratin 15	NM_008469	+ 3.8
Fmo3	flavin containing monooxygenase 3	NM_008030	+ 3.7
Esrrg	estrogen-related receptor gamma	NM_011935	+ 3.7
Upk1b	uroplakin 1B	NM_178924	+ 3.6
Myo5c	myosin VC	BC003985	+ 3.4
9530003J23Rik	RIKEN cDNA 9530003J23 gene	NM_029906	+ 3.2
Pkp1	plakophilin 1	NM_019645	+ 3.1
LOC546176	Similar to Spindlin-like protein 2 (SPIN-2)	XM_620811	+ 3.0
Tmprss2	transmembrane protease, serine 2	NM_015775	+ 3.0
2210407C18Rik	RIKEN cDNA 2210407C18 gene	NM_144544	+ 3.0
EG639426	similar to Tetratricopeptide repeat protein 6	XR_003227	+ 2.9
Rnmt	RNA (guanine-7-) methyltransferase	AK084393	+ 2.9
Krt5	keratin 5	NM_027011	+ 2.8
Ptprk	protein tyrosine phosphatase, receptor type, K	AK078614	+ 2.6
Cd209b	CD209b antigen	NM_026972	+ 2.6
Sell13	sel-1 suppressor of lin-12-like 3	NM_172710	+ 2.6
Sox9	SRY-box containing gene 9	NM_011448	+ 2.6
Bdnf	brain derived neurotrophic factor	NM_007540	+ 2.4
4933407L21Rik	RIKEN cDNA 4933407L21 gene	AK016730	+ 2.4
B930041F14Rik	RIKEN cDNA B930041F14 gene	NM_178699	+ 2.4
Prtg	protogenin homolog	AK036172	+ 2.3
Apod	apolipoprotein D	NM_007470	+ 2.3
Olfir971	olfactory receptor 971	NM_146614	+ 2.3
Cyr61	cysteine rich protein 61	NM_010516	+ 2.3
Npy2r	neuropeptide Y receptor Y2	NM_008731	+ 2.2
Grhl1	grainyhead-like 1	NM_145890	+ 2.2
Ric3	resistance to inhibitors of cholinesterase 3	NM_001038624	+ 2.2
5031410I06Rik	RIKEN cDNA 5031410I06 gene	NM_207657	+ 2.2
Pcdhga1	protocadherin gamma subfamily A, 1	NM_033584	+ 2.2
Pigr	polymeric immunoglobulin receptor	NM_011082	+ 2.2
Cpne5	copine V	NM_153166	+ 2.2
Cyt11	cytokine like 1	BC063103	+ 2.2
Slc6a7	solute carrier family 6, member 7	NM_201353	+ 2.2
Dsp	desmoplakin	AK077574	+ 2.2
Gjb3	gap junction membrane channel protein beta 3	NM_008126	+ 2.1
4930591A17Rik	RIKEN cDNA 4930591A17 gene	NM_026596	+ 2.1
Edg4	endothelial diff. lysophosphatidic acid GPCR 4	NM_020028	+ 2.1
Faim2	Fas apoptotic inhibitory molecule 2	NM_028224	+ 2.1

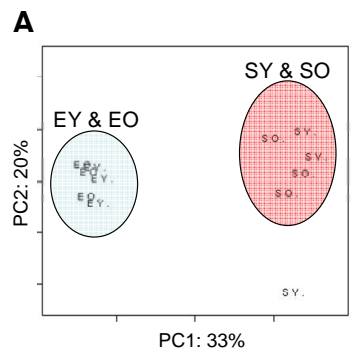
Microarray analysis of gene expression in microdissected mouse prostate stroma from old (24 month) compared to young (4 month) C57BL/6 mice. Unique genes (n=53) with significantly increased transcript levels between aged and young samples ($p < 0.05$) and whose expression levels were low in white blood cells. Fold changes were calculated from the averages across multiple anterior and dorsal prostate samples in each group. Positive values indicate an increase in gene expression in aged prostate as compared to young.

Table 2. Genes with lower in expression in the mouse prostate stroma from old (24 months) compared to young (4 months) C57BL/6 mice.

<i>Gene symbol</i>	<i>Gene name (abbreviated)</i>	<i>GenBank accession</i>	<i>Fold change (old/young)</i>
Lrat	lecithin-retinol acyltransferase	NM_023624	-4.4
Uxs1	UDP-glucuronate decarboxylase 1	AK078575	-4.2
A930025H08Rik	RIKEN cDNA A930025H08 gene	AK020889	-3.8
Adams19	ADAM with thrombospondin type 1 motif, 19	NM_175506	-3.7
Nrxn1	neurexin I	NM_020252	-3.6
6530401D17Rik	RIKEN cDNA 6530401D17 gene	NM_029541	-3.3
2900006F19Rik	RIKEN cDNA 2900006F19 gene	NM_028387	-3.2
D930015E06Rik	RIKEN cDNA D930015E06 gene	AK153996	-3.1
Prnd	prion protein dublet	NM_023043	-3.1
Atp1b3	ATPase, Na ⁺ /K ⁺ transporting, beta 3	AK078587	-3.1
5730507A11Rik	RIKEN cDNA 5730507A11 gene	AK020490	-3.0
Abhd2	abhydrolase domain containing 2	NM_018811	-3.0
Sox11	SRY-box containing gene 11	AF009414	-3.0
C630004L07	hypothetical protein C630004L07	AK049864	-2.9
Nfrkb	nuclear factor related to kappa B binding	AK036381	-2.8
Zfp715	zinc finger protein 715	AK011730	-2.7
Grik4	glutamate receptor, ionotropic, kainate 4	NM_175481	-2.7
EG621699	similar to 40S ribosomal protein S7 (S8)	AK048878	-2.7
Fzd3	frizzled homolog 3	NM_021458	-2.6
4833446K15Rik	RIKEN cDNA 4833446K15 gene	XM_894542	-2.6
Gdap1	ganglioside-induced diff. associated-protein 1	NM_010267	-2.6
Calcb	calcitonin-related polypeptide, beta	NM_054084	-2.5
Pde11a	phosphodiesterase 11A	AK050924	-2.5
Cacna1g	calcium channel, volt. dep., T type, alpha 1G	NM_009783	-2.4
Fbxo7	F-box only protein 7	BC059894	-2.4
Ccdc106	coiled-coil domain containing 106	NM_146178	-2.4
Colla1	procollagen, type I, alpha 1	NM_007742	-2.4
Pcdhb4	protocadherin beta 4	NM_053129	-2.3
BC068157	cDNA sequence BC068157	NM_207203	-2.3
Bub1	budding uninhibited by benzimidazoles 1	NM_009772	-2.2
Tomm70a	translocase of outer mitoc. membrane 70 A	AK122356	-2.2
LOC665113	similar to Traf2 and NCK-interacting kinase	XM_976833	-2.2
Ppp2r2b	protein phosphatase 2, regulatory subunit B	NM_028392	-2.1
Bub3	budding uninhibited by benzimidazoles 3	AK083742	-2.1
Kif4	kinesin family member 4	NM_008446	-2.1
Pcdhb7	protocadherin beta 7	NM_053132	-2.1
Fgf12	fibroblast growth factor 12	NM_183064	-2.1
Plxna3	plexin A3	AK049319	-2.1
Tmem121	transmembrane protein 121	NM_153776	-2.1
Epb4.113	erythrocyte protein band 4.1-like 3	AK086340	-2.1

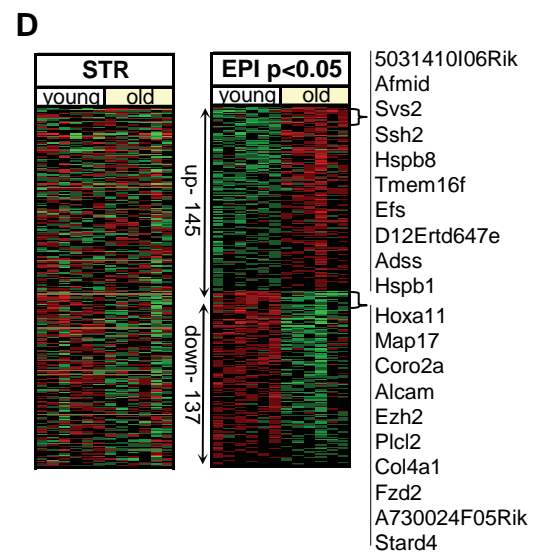
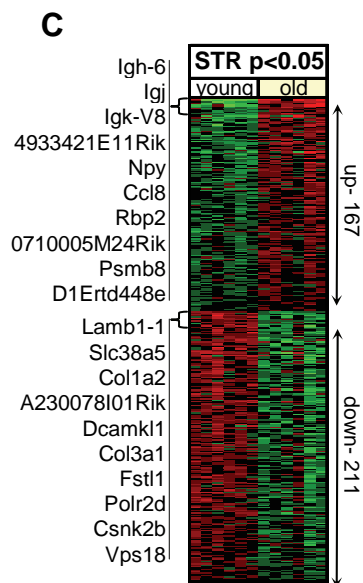
Microarray analysis of gene expression in microdissected mouse prostate stroma from old (24 months) compared to young (4 months) C57BL/6 mice. Unique genes (n=40) with significantly lower expression in aged compared to young samples ($p<0.05$) and whose expression levels were also low in white blood cells. Fold changes were calculated from the averages across multiple anterior and dorsal prostate samples in each group. Negative values indicate a decrease in gene expression in aged prostate as compared to young.

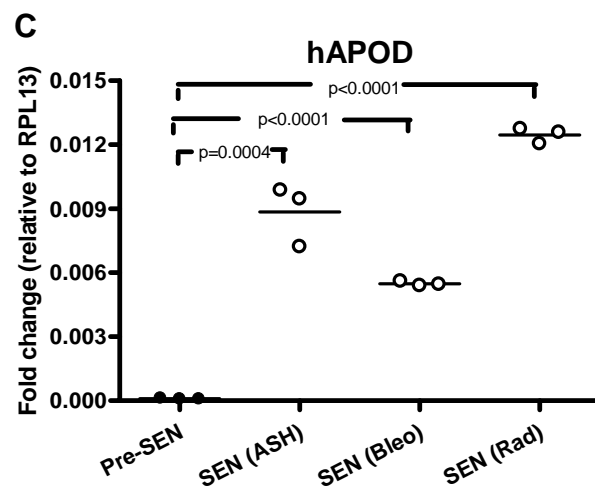
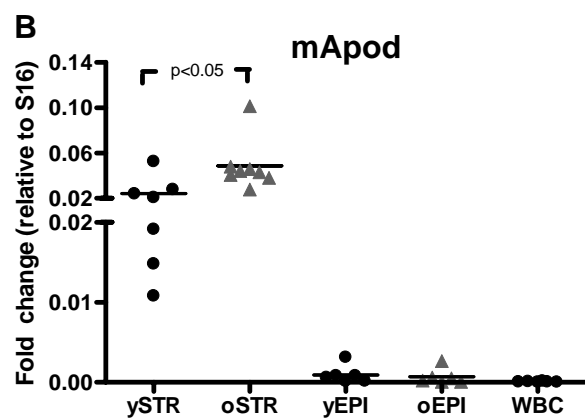
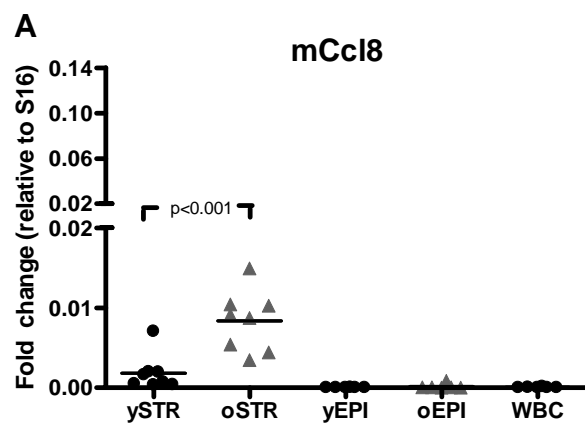




B

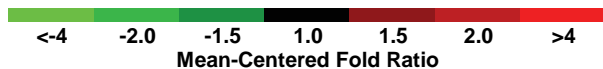
	HUGO	Description	Stroma				Epithelium			
			yDP	yAP	oDP	oAP	yDP	yAP	oDP	oAP
STR	Actg2	Actin gamma 2								
	Acta1	Actin alpha 1								
	Acta2	Actin alpha 2								
	Myh11	Myosin heavy chain 11								
	Vcl	Vinculin								
	Des	Desmin								
EPI	Vim	Vimentin								
	Pbsn	Probasin								
	Krt1-18	Keratin 18								
	Nkx3-1	NK-3 transcription factor								





A

Gene symbol	ySTR		oSTR		WBC
	yAPS	yDPS	oAPS	oDPS	
0710005M24Rik					
Ccl8					
Apod					
Fmo3					
BC020489					
Cyr61					
Bdnf					
Ccl12					
4933407L21Rik					
Prtg					
Upk1b					
Ptpk					
B930041F14Rik					
Esrrg					
Slc26a3					
5330417C22Rik					
Krt15					
Gylt1b					
Serpinb5					
2310045A20Rik					
LOC432593					
Krt5					
Pkp1					
Tmprss2					
2210407C18Rik					
9530003J23Rik					
Trp63					
Fcgbp					
EG639426					
Sox9					
Myo5c					
Col17a1					
LOC546176					
Coch					
Cd209b					
Rnmt					
Olf971					
Trim9					
Nefh					



B

Gene symbol	ySTR		oSTR		WBC
	yAPS	yDPS	oAPS	oDPS	
C130026I21Rik					
Gbp4					
Ccl5					
Cd8b1					
Zfp26					
Ccl7					
A530040E14Rik					
Cd8a					
Il7r					
Eif4enif1					
Cd38					
C3ar1					
Ptpn22					
Fos					
Slco4a1					
Atf3					
6330437E22Rik					
Egr3					
Ccl4					
Arc					
Nlr4					
Thbs1					
Ifng					
Nr4a1					
2010016I18Rik					
Ccl3					
EG433637					
Cd84					
Igk-V38					
Runx2					
Rhoh					
Faim3					
Igl-V1					
Txndc11					
Slamf6					
Tspan1					
Tgm4					
Ms4a5					
Cdh1					
Mmp7					
Atp6v1c2					
Agr2					

